

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2004, 11:50:08 ; Search time 114.64 Seconds

(without alignments)  
2416.469 Million cell updates/sec

Title: US-09-937-908-1

Perfect score: 4675

Sequence: 1 MFGIGKNIIEGALNTTGDLA.....LVFSSNEGLTGRGIPNSISI 878

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_podent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4675	100.0	878	10	Q42710
2	4672	99.9	878	10	Q42704
3	3657.5	78.2	877	10	Q42705
4	3038	65.0	873	10	Q93Y18
5	2992.5	64.0	857	10	Q41238
6	2862	63.8	860	10	Q41238
7	2959	63.3	864	10	Q49150
8	2948.5	63.1	862	10	Q43191
9	2946	63.0	862	10	Q9FT17
10	2942.5	62.9	862	10	Q9LEA9
11	2941	62.9	861	10	Q24379
12	2939	62.9	861	10	Q22508
13	2936	62.8	861	10	Q9SC16
14	2931.5	62.7	862	10	Q8W4X6
15	2925	62.6	861	10	Q22507
16	2917	62.4	861	10	Q43189

#### ALIGNMENTS

#### RESULT 1

Q42710	Q42710	PRELIMINARY;	PRT;	878 AA.
ID	Q42710	PRELIMINARY;	PRT;	878 AA.
AC	Q42710;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Lipoxigenase (EC 1.13.11.12).			
OS	Cucumis sativus (Cucumber).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid1; Cucurbitales; Cucurbitaceae; Cucumis.			
OX	NCBI_TaxID=3659;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cotyledon;			
RX	MEDLINE=97054584; PubMed=898881;			
RA	Hoehne M., Nellen A., Schwennesen A., Kindl H.;			
RT	"Lipid body lipoxigenase characterized by protein fragmentation, cDNA			
RT	sequence and by its very early expression during germination of			
RT	cucumber seeds.";			
RL	Eur. J. Biochem. 241:6-11(1996).			
DR	EMBL; X92890; CAA63483.1; -.			
DR	P1R; S74207; S74207.			
DR	HSSP; P08170; 2SBL.			
DR	GO; GO:0005506; F:iron ion binding; IEA.			
DR	GO; GO:0016165; F:lipoxigenase activity; IEA.			
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.			
DR	GO; GO:0006118; P:electron transport; IEA.			
DR	InterPro; IPR000907; Lipoxigenase.			
DR	InterPro; IPR01024; Lipoxigenase_LH2.			
DR	Pfam; PF00305; lipoxigenase; 1.			
DR	Pfam; PF01477; PLAT; 1.			
DR	PRINTS; PR00087; LIPOXYGENASE.			
DR	SMART; SM00308; LH2; 1.			
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.			
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.			
DR	PROSITE; PS00095; PLAT; 1.			

17	2916	62.4	844	10	Q9SAP1	Q9sap1 solanum tub
18	2911	62.3	862	10	Q43800	Q43800 nicotiana t
19	2895.5	61.9	865	10	Q93W22	Q93w22 gossypium h
20	2876.5	61.5	884	10	Q7X9G5	Q7x9g5 fragaria an
21	2876	61.5	857	10	Q8GV02	Q8gv02 brassica na
22	2813.5	60.2	859	10	Q42873	Q42873 lycopersico
23	2762	59.1	881	10	Q9M463	Q9m463 cucumis sat
24	2705	57.9	876	10	Q41430	Q41430 solanum tub
25	2692.5	57.6	866	10	Q39870	Q39870 glycine max
26	2677.5	57.3	854	10	Q9FNF7	Q9fnf7 arabidopsis
27	2677.5	57.3	858	10	Q9ZU05	Q9zu05 persea aner
28	2663	57.0	865	10	Q24320	Q24320 phaseolus v
29	2653.5	56.8	882	10	Q9LUW0	Q9luw0 arabidopsis
30	2649	56.7	859	10	Q43440	Q43440 glycine max
31	2640.5	56.5	858	10	Q04919	Q04919 vicia faba
32	2634.5	56.4	856	10	Q24780	Q24780 glycine max
33	2632.5	56.3	868	10	Q24470	Q24470 pisum sativ
34	2577	55.1	853	10	Q43446	Q43446 glycine max
35	2571	55.0	839	10	Q43438	Q43438 glycine max
36	2567	54.9	866	10	Q24295	Q24295 pisum sativ
37	2552.5	54.6	856	10	Q9M684	Q9m684 phaseolus v
38	2538.5	54.3	877	10	Q8S6D6	Q8s6d6 cryza sativ
39	2536.5	54.3	874	10	Q9FQF9	Q9fqf9 phaseolus v
40	2531	54.1	863	10	Q8S6E8	Q8s6e8 cryza sativ
41	2529	54.1	865	10	Q9FEQ3	Q9feg3 pisum sativ
42	2525.5	54.0	864	10	Q8W0V2	Q8w0v2 zea mays (m
43	2522.5	54.0	864	10	Q9AXG8	Q9axg8 zea mays (m
44	2518.5	53.9	697	10	Q24377	Q24377 solanum tub
45	2507	53.6	870	10	Q7Y1F4	Q7y1f4 cryza sativ

KW OXidoreductase.  
SQ SEQUENCE 878 AA; 99768 MW; A92660AFA4D1ED3BE CRC64;  
Query Match 100.0%; Score 4675; DB 10; Length 878;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGIGKNIIEGALNTTGLAGSVINAGNIIIDRVSSLGKNGKAYLERWLSIIPPLFAGESVFOINF 60  
DB 1 MFGIGKNIIEGALNTTGLAGSVINAGNIIIDRVSSLGKNGKAYLERWLSIIPPLFAGESVFOINF 60

QY 61 SNLLDNFTLLGGGVSFOLISATHTSNDNRGKNGKAYLERWLSIIPPLFAGESVFOINF 120  
DB 61 SNLLDNFTLLGGGVSFOLISATHTSNDNRGKNGKAYLERWLSIIPPLFAGESVFOINF 120

QY 121 QWENFGFPGAFFIKNGHTSEFFLKSLLTDVPGVGRVHFDNCNSWVPSGRYKDDRIFFA 180  
DB 121 QWENFGFPGAFFIKNGHTSEFFLKSLLTDVPGVGRVHFDNCNSWVPSGRYKDDRIFFA 180

QY 181 NHVYLPSTQTPNPLRYKREELWNLRGDTGERKEWDRIYDVYNDIADPDVGDHRPILG 240  
DB 181 NHVYLPSTQTPNPLRYKREELWNLRGDTGERKEWDRIYDVYNDIADPDVGDHRPILG 240

QY 241 GTTEYPYPRRGRTGPRSRDRHNYESRSLPMSLDIYVPKDNFGLKMSDFLGYTLKAL 300  
DB 241 GTTEYPYPRRGRTGPRSRDRHNYESRSLPMSLDIYVPKDNFGLKMSDFLGYTLKAL 300

QY 301 SISIKPGLQSIQFVTPNPFNFKEVDNLFERGFPIPFNAFKTLTETDTPPLFKALVRNDG 360  
DB 301 SISIKPGLQSIQFVTPNPFNFKEVDNLFERGFPIPFNAFKTLTETDTPPLFKALVRNDG 360

QY 361 EKFLKFTPEVVKONKIGWSTDEFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420  
DB 361 EKFLKFTPEVVKONKIGWSTDEFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420

QY 421 TITEHIIKHGDLGLTVDSAMQNRLIYVDFHDLMPYLTRNATSTKYATRTLLLLKDD 480  
DB 421 TITEHIIKHGDLGLTVDSAMQNRLIYVDFHDLMPYLTRNATSTKYATRTLLLLKDD 480

QY 481 GTLKLPLVIELALPHFQDGLGAIKSLYPPAENGQKSIWQLAKAYTVNDVGVHQLISHW 540  
DB 481 GTLKLPLVIELALPHFQDGLGAIKSLYPPAENGQKSIWQLAKAYTVNDVGVHQLISHW 540

QY 541 LHTHAVLEPFIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLINAGLIETHTYPS 600  
DB 541 LHTHAVLEPFIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLINAGLIETHTYPS 600

QY 601 KYSBELSILYKDWTFPQDALPNNLMKGLAVEDSSAPHGLRLILINDYPAVDGLDIWSA 660  
DB 601 KYSBELSILYKDWTFPQDALPNNLMKGLAVEDSSAPHGLRLILINDYPAVDGLDIWSA 660

QY 661 IKTWQDYCCLYKDDNVAQNDVFLQSWNBLREKSHADKKHEPWPWPMQOTSELIBSCT 720  
DB 661 IKTWQDYCCLYKDDNVAQNDVFLQSWNBLREKSHADKKHEPWPWPMQOTSELIBSCT 720

QY 721 TIITWASALHAANFQVPGYGYILNRPTTSGRRFMPVGTAEYKELESNPEKAFPLRTICS 780  
DB 721 TIITWASALHAANFQVPGYGYILNRPTTSGRRFMPVGTAEYKELESNPEKAFPLRTICS 780

QY 781 ELQALVSIISIIELSKHASDVYLGQASIDWTSKDIALEAFKGNLFEVENRIMERN 840  
DB 781 ELQALVSIISIIELSKHASDVYLGQASIDWTSKDIALEAFKGNLFEVENRIMERN 840

QY 841 KEVNLKNSGPNLPYTLVLPSSNEGLTGRGIPNSISI 878  
DB 841 KEVNLKNSGPNLPYTLVLPSSNEGLTGRGIPNSISI 878

RESULT 2  
Q42704  
ID Q42704 PRELIMINARY; PRT; 878 AA.  
AC Q42704;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
GN Lipoxxygenase 1 (EC 1.13.11.12).  
OS Cucumis sativus (Cucumber).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
OX NCBI\_taxid=3659;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Suvo; TISSUE=Germinating cotyledons;  
RX MEDLINE=96061722; PubMed=7480330;  
RA Matsui K., Tsuru E., Kajiwara T., Hase T.;  
RT "Nucleotide sequence of a cucumber cotyledon lipoxxygenase cDNA  
GenBank U25058 (F0935-044).";  
RL Plant Physiol. 109:337-337(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Suvo; TISSUE=Germinating cotyledons;  
RA Matsui K., Tsuru E., Kajiwara T., Hase T.;  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U25058; AAC61785.1; -.  
DR HSSP; P08170; 2SBL.  
DR GO; GO:0005506; F:Iron ion binding; IEA.  
DR GO; GO:0016165; F:lipoxxygenase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR000907; Lipoxxygenase\_LH2.  
DR InterPro; IPR001024; Lipoxxygenase\_LH2.  
DR InterPro; IPR008976; PLAT\_LH2.  
DR Pfam; PF00305; lipoxxygenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00881; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS00095; PLAT; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 878 AA; 99784 MW; F219407ED7C269B8 CRC64;  
Query Match 99.9%; Score 4672; DB 10; Length 878;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 877; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGIGKNIIEGALNTTGLAGSVINAGNIIIDRVSSLGKNGKAYLERWLSIIPPLFAGESVFOINF 60  
DB 1 MFGIGKNIIEGALNTTGLAGSVINAGNIIIDRVSSLGKNGKAYLERWLSIIPPLFAGESVFOINF 60

QY 61 SNLLDNFTLLGGGVSFOLISATHTSNDNRGKNGKAYLERWLSIIPPLFAGESVFOINF 120  
DB 61 SNLLDNFTLLGGGVSFOLISATHTSNDNRGKNGKAYLERWLSIIPPLFAGESVFOINF 120

QY 121 QWENFGFPGAFFIKNGHTSEFFLKSLLTDVPGVGRVHFDNCNSWVPSGRYKDDRIFFA 180  
DB 121 QWENFGFPGAFFIKNGHTSEFFLKSLLTDVPGVGRVHFDNCNSWVPSGRYKDDRIFFA 180

QY 181 NHVYLPSTQTPNPLRYKREELWNLRGDTGERKEWDRIYDVYNDIADPDVGDHRPILG 240  
DB 181 NHVYLPSTQTPNPLRYKREELWNLRGDTGERKEWDRIYDVYNDIADPDVGDHRPILG 240

QY 241 GTTEYPYPRRGRTGPRSRDRHNYESRSLPMSLDIYVPKDNFGLKMSDFLGYTLKAL 300  
DB 241 GTTEYPYPRRGRTGPRSRDRHNYESRSLPMSLDIYVPKDNFGLKMSDFLGYTLKAL 300

QY 301 SISIKPGLQSIQFVTPNPFNFKEVDNLFERGFPIPFNAFKTLTETDTPPLFKALVRNDG 360  
DB 301 SISIKPGLQSIQFVTPNPFNFKEVDNLFERGFPIPFNAFKTLTETDTPPLFKALVRNDG 360

QY 361 EKFLKFTPEVVKONKIGWSTDEFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420  
DB 361 EKFLKFTPEVVKONKIGWSTDEFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420

```

QY 421 TITTEHIKHGLDGLTVDEAMKQNLVYVDFHDMPLVTRMNTSTTKYATRTLLLLKOD 480
DB 421 TITTEHIKHGLDGLTVDEAMKQNLVYVDFHDMPLVTRMNTSTTKYATRTLLLLKOD 480
QY 481 GTLKLPLVIELALPHPOGDLGAIKSLYFPAENGVOKSIWOLAKAYVTVNDVGVHQLISHW 540
DB 481 GTLKLPLVIELALPHPOGDLGAIKSLYFPAENGVOKSIWOLAKAYVTVNDVGVHQLISHW 540
QY 541 LHTHAUVEFPFVIATHRQLSVLHPHKLVLPHYKDTMFINASAROVLINANGLIETTHYPS 600
DB 541 LHTHAUVEFPFVIATHRQLSVLHPHKLVLPHYKDTMFINASAROVLINANGLIETTHYPS 600
QY 601 KYSNELSILYKDMTFDQALPNNLMKRGLAVEDSSAPHGRLRLINDYPAVGLDLSWA 660
DB 601 KYSNELSILYKDMTFDQALPNNLMKRGLAVEDSSAPHGRLRLINDYPAVGLDLSWA 660
QY 661 IKTWVQDYCCLYYKDDNAVQNDFELQSWNELREKGHADKKEHPWPKMTLSSELIESCT 720
DB 661 IKTWVQDYCCLYYKDDNAVQNDFELQSWNELREKGHADKKEHPWPKMTLSSELIESCT 720
QY 721 TIIMIASALHAAVNFGQYPYGGYILNRPPTTSRRPMPVGTAEYKELESNEPEKAFRTICS 780
DB 721 TIIMIASALHAAVNFGQYPYGGYILNRPPTTSRRPMPVGTAEYKELESNEPEKAFRTICS 780
QY 781 ELQALVSIISIEILSKHASDEVILGQASIDWTSDKIALFAFEKFGKNLFEVENRIMERN 840
DB 781 ELQALVSIISIEILSKHASDEVILGQASIDWTSDKIALFAFEKFGKNLFEVENRIMERN 840
QY 841 KEVNLKNSGPNVLPYLLVPSNEGTLGRGIPNSISI 878
DB 841 KEVNLKNSGPNVLPYLLVPSNEGTLGRGIPNSISI 878

```

## RESULT 3

```

Q42705 PRELIMINARY; PRT; 877 AA.
ID Q42705
AC Q42705;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI TaxID=3659;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=Suoyo; TISSUE=Root;
RA Matsui K., Nishiooka M., Kajiwara T., Hase T.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U36339; AAA79186.1; -
DR PIR; T10085; T10085.
DR HSSP; P09186; 1LNH.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0004615; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Oxidoreductase.
SQ
SEQUENCE 877 AA; 99393 MW; 3EL7B89719FA33F CRC64;

```

Query Match

Best Local Similarity

78.2%; Score 3657.5; DB 10; Length 877;  
76.2%; Pred. No. 6.7e-265;

```

Matches 671; Conservative 105; Mismatches 99; Indels 5; Gaps 4;
QY 1 MFGIGKNIIEGALNTTGLAGSVINAGGNILDRVSSLGNGKIKGVILMRSNVLDFTFFH 60
DB 1 MFSIGKNIIEGALNTTGLAGSVINAGGNIAQDISNIGGQKIKGVILMRSNVMDFTFFH 60
QY 61 SNLONFTELLGGGVFSQLISATHTSN-DSRGKVGKAYLERWLTSLIPPLFAGESVPQIN 119
DB 61 SELLONFTELLGGGVFSQLISATQTSALDSRGKVGKAFLEWLTSLIPPLFAGESVFOVS 120
QY 120 FOWDENFGPGGAFFIKNGHTSEFFLKSITLDDVPYGRVHFDCNSWVPSGYSKDRIF 179
DB 121 FWESEFGPGGAFFIKNGHTSEFFLKSITLDDVPYGRVHFDCNSWVPSGYSKDRIF 180
QY 180 ANHYVLPSTPNPLKRYREELWNLURGDGTGERKWDRIYDYVDVNDIADPDVGHRPIL 239
DB 181 ANNYVLPSTPNPLKRYREELWNLURGDGTGERKWDRIYDYVDVNDIADPDVGHRPIL 238
QY 240 GGTTEVPYPRRGRTGRPRSRDRHYESRLSPIMSLDIYVPKDNFGLKMSDFLYTLKA 299
DB 239 GG-SQFPYPRRGRTGRPREWKSNSYERLPPVSGLNIVPRDENFGLKMSDFLYTLKA 297
QY 300 LSISIKPGLQSIPIDVTPNEFDNFKVDNLFERGPIPFNAFKLTLEDTPPLFKALVRND 359
DB 298 LVATVQPALVNIIVDTFGDFKFDVHNLVEGGLVPLDVFENLTGFTPPMFQELLRTD 357
QY 360 G-EKELKFTPEWVKDNKIGNSTDEEFAREMLAGNPILLIRLEAFPTSKLDPMVGNQ 418
DB 358 NDORFLKFSPPQVVRKEDKPAWQTDDEFAREMLAGNPILLIRLEAFPTSKLDPMVGNQ 417
QY 419 NSTITTEHIKHGLDGLTVDEAMKQNLVYVDFHDMPLVTRMNTSTTKYATRTLLLLK 478
DB 418 HSKITEEDIKSGLEGLTVAEALNQRLYILDHDMALPRLKINSTKTATRTLLLLK 477
QY 479 DDGTLKPLVIELALPHPOGDLGAIKSLYFPAENGVOKSIWOLAKAYVTVNDVGHQLIS 538
DB 478 NDGTLKPLVIELALPHPOGDLGAIKSLYFPAENGVOKSIWOLAKAYVTVNDVGHQLIS 537
QY 539 HMLTHAVLEPFIATHRQLSVLHPHKLVLPHYKDTMFINASAROVLINANGLIETTHY 598
DB 538 HMLTHAVLEPFIATHRQLSVLHPHKLVLPHYKDTMFINASAROVLINANGLIETTHY 597
QY 599 PKYINELSSILYKDMTFDQALPNNLMKRGLAVEDSSAPHGRLRLINDYPAVGLDLSW 658
DB 598 QSKYAMELSSYTYKEWNFTQALPVDLIKRGVAVEDPSPNGVKLLIEDYPAVGLDLSW 657
QY 659 SALKTWQDYCCLYYKDDNAVQNDFELQSWNELREKGHADKKEHPWPKMTLSSELIES 718
DB 658 STIKTWVNYCSLYYKDDSAIQNDVELQSWKEVREKGVKDKNETWPKQNFNVELVET 717
QY 719 CTIIIIWIASALHAAVNFGQYPYGGYILNRPPTTSRRPMPVGTAEYKELESNEPEKAFRTI 778
DB 718 CTIIIIWIASALHAAVNFGQYPYGGYILNRPPTTSRRPMPVGTAEYKELESNEPEKAFRTI 777
QY 779 CSELQALVSIISIEILSKHASDEVILGQASIDWTSDKIALFAFEKFGKNLFEVENRIME 838
DB 778 NSMLQTLGVSLIETLSRHSASDEVILGQASIDWTSDKIALFAFEKFGKNLFEVENRIME 837
QY 839 RNKEVNLKNSGPNVLPYLLVPSNEGTLGRGIPNSISI 878
DB 838 RNKVDNKLKNSGPNVLPYLLVPSNEGTLGRGIPNSISI 877

```

## RESULT 4

```

Q93YI8 PRELIMINARY; PRT; 873 AA.
ID Q93YI8
AC Q93YI8;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
OX NCBI TaxID=3659;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=Suoyo; TISSUE=Root;
RA Matsui K., Nishiooka M., Kajiwara T., Hase T.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U36339; AAA79186.1; -
DR PIR; T10085; T10085.
DR HSSP; P09186; 1LNH.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0004615; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Oxidoreductase.
SQ
SEQUENCE 877 AA; 99393 MW; 3EL7B89719FA33F CRC64;

```

Query Match

Best Local Similarity

78.2%; Score 3657.5; DB 10; Length 877;  
76.2%; Pred. No. 6.7e-265;





Db 127 DVNKGKVFVNCNWSVYPSFRYSKSDRIFFANQPYLPSETPELLAKRYENELLTLRGDGTG 186  
Qy 211 ERKEWDRIYDVNDIADPDVGH--RPILGGTTEYPPRGSTGRPRSRDNYESRL 268  
Db 187 KREAWDRYDVNDLNGDQGEQNVTTGGGADYPPRRGTGPRPTDPKSESRI 246  
Qy 269 SPIMSLDIYVPRDKNFGLKMSDFLGYTLKALSISIKPGLQSIQFDVTPNFFDNFKEDNL 328  
Db 247 PLILSLDIYVPRDERFGLKMSDFLTVALKISIQVFIPLPELHALFDGTPNEFDSFEDVLR 306  
Qy 329 FERGPPIFN-AFKTLTIEDTPPLFKALVRNDGKFLKFPPEVVKNKICGWSDEBFAR 387  
Db 307 YEGGKLFQGBLFKALTAAPLEMMKELLRTDGEILRFPPLVKDSKTAMRWDEBFAR 366  
Qy 388 EMLAGNELLIRLEAFPPSKLPNVYGNQNSITTEHIIKHGDLGLTVDEAMKONRLXI 447  
Db 367 EMLAGNVLIIISRLQEPFPKSLDPEAYGNQNSITTAHIEDKLDGLTVDEAMNNKLF 426  
Qy 448 VDFHDLMPYITRMNASTKYATRTLLLLKDDGTLPVLTELALPHQDGLGALSILY 507  
Db 427 LNHHDLIPYLRRINTTTKTYASRTLLFLQDNGSLKPLATELSLPHDPDQGFQVISKVY 486  
Qy 508 FPAENGOKSIWQAKAYVTVNDVGYHQLISHWLTHAVLEPPFVIATHROLVLHPHKL 567  
Db 487 TPSQGVESSIWQAKAYVAVNDVSGVHQLISHWLTHAVLEPPFVIATHROLVLHPHKL 546  
Qy 568 LVPHYKDTMFINASARQVLINANGLIETHYPSKYSMELSSILYKDWTFPDQALPNNLMK 627  
Db 547 LYPHFRDTMFINAMARQILINAGGVLESTVFPKFAVMSAVYKDWVFPDQALPADLVK 606  
Qy 628 RGLAVEDSSAPHLRLINDYPAVDGLDITWSAKITWVODYCCLYKDDNAVQDFLOS 687  
Db 607 RGVAVEDSSSPHGKLLIEDIPYAVDGLIEIWSAKITWVODYCCLYKDDNAVQDFLOS 666  
Qy 688 WNNELREKGHADKKEHPMPKXQMTLSIELIBSCTTIIWIASALHAANVFGQVPGYILNR 747  
Db 667 WKELREVGCHGDKNEPMPWEVETPQELIDSCITIIWIASALHAANVFGQVPGYILNR 726  
Qy 748 PTTSRFPPEVGTAEYKELESNPKAFRTICSELOALVSIISIIILSKHASDEVYLGQR 807  
Db 727 PTVSRFPPEVGTAEYKELESNPKAFRTICSELOALVSIISIIILSKHASDEVYLGQR 786  
Qy 808 ASIOWTSKIALAEAFKGNLPEVNRIMERNKEVNLKNSGPNVLPYLLVPSSNEGL 867  
Db 787 ESPWTKDKEPLAADFEGKLLDIEKQIQRNGDNILTRSGVGNAPYLLPFTSBGGL 846  
Qy 868 TGRGIPNSISI 878  
Db 847 TKGIPNSVSI 857

## RESULT 6

Q43190 ID Q43190 PRELIMINARY; PRT; 860 AA.  
AC DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
CD 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Lipoxigenase (EC 1.13.11.12).  
GN Polix-2.  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamids; Solanales; Solanaceae; Solanum.  
OC NCBI\_taxID=4113;  
EN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Superior;  
RA Kolomets M.V., Hannapel D.J., Gladon R.J.;  
RT "Potato Lipoxigenase Genes Expressed During the Early Stages of  
RT Tubarization (Accession Nos. U60200 and U60201) (F0996-065).";  
RL Plant Physiol. 112:446-446(1996).  
DR EMBL; U60201; AB67860.1; --

DR HSSP; P08170; 2SBL.  
DR GO; GO:000506; F-iron ion binding; IEA.  
DR GO; GO:0016165; F-lipoxygenase activity; IEA.  
DR GO; GO:0016491; F-oxidoreductase activity; IEA.  
DR GO; GO:0006118; P-electron transport; IEA.  
DR InterPro; IPR000907; Lipoxygenase.  
DR InterPro; IPR001024; Lipoxygenase\_LH2.  
DR InterPro; IPR008976; PLAT LH2.  
DR Pfam; PF00305; lipoxygenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS50095; PLAT; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 860 AA; 96969 MW; 11FD0D769921053E CRC64;

Query Match 63.8%; Score 2982; DB 10; Length 860;  
Best Local Similarity 63.8%; Pred. No. 2.7e-214;  
Matches 553; Conservative 125; Mismatches 175; Indels 14; Gaps 5;

Qy 17 GDLAGSVINAGNILDVSSLOGNKKGVILMRNVLDFTFHSNLLDNFTTELLGGVVS 76  
Db 3 GOIVGGLI--GGH-----HDSKKVKTVMKKKXNLDFTDLAGSLDKIFEALGQKVS 53  
Qy 77 FQLISATHT--SNDGRGKVGKAYLERMLTISIPPLFAGESVFOINQFOWDENFGFPAPFI 134  
Db 54 FQLISSVQSDPANGUQGHSHNAYLENFLFITPLAAGETAAGVTDFWNEEFGVCGATII 113  
Qy 135 KNGHTSEFPLKSLTLDVPGYGRVHFDNCNWSVYPSGRYKKDRIFFANHYVLPSCPNPLR 194  
Db 114 KNTHINEFFKSLTLEDVPHNGKHFVNCNWSVYPSFRYSKSDRIFFANQPYLPSETPELL 173  
Qy 195 KYREELNLRGDGGERKEWDRIYDVYNDIADPDVGH--RPILGGTTEYPPRGGR 252  
Db 174 KYREELLTLRGDGTGKEAWDRIYDVYNDLGNPDQCKENVRITLGGSDADYPPRGGR 233  
Qy 253 TGRPSRRDNYESRLSDIYVPKDNFPHLKNSDFLGYTLKALSISIKPGLQSI 312  
Db 234 TGRPPTRTDPKSESRIPLISLDIYVPRDERFGLKMSDFLTVALKISIQVFIPLPELHALF 293  
Qy 313 DVTNEFDNFKEVDNLFERGPPIPN-AFKTLTIEDTPPLFKALVRNDGKFLKFPPEV 371  
Db 294 DGTNEFDSFEDVLRLEGGIRLPQGLFKALTDAIPELMIRELRLTDEGILREPTPLV 353  
Qy 372 VKDNKIGSTDEEFAREMLAGNPLILIRLEAFPPSKLPDNVYGNQNSITTEHIIKHGL 431  
Db 354 IKDSKTAWRTDEEFAREMLAGNPNIIISRLQEPFPKSLDPEAYGNQNSITTAHIEDKL 413  
Qy 432 DGLTVDEAMKONRLXIYVDFHDLMPYITRMNASTKYATRTLLLLKDDGTLPVLIELA 491  
Db 414 DGLTVDEAMNNKLPILNHHDLVLIPLYRRINTTTKTYASRTLLFLQDNGSLKPLATELS 473  
Qy 492 LPHPOGDOLGALSILYFPAENGOKSIWQAKAYVTVNDVGYHQLISHWLTHAVLEPPV 551  
Db 474 LPHPOGDQFGVTSKYITTSQGVESSIWQAKAYVAVNDVSGVHQLISHWLTHAVLEPPV 533  
Qy 552 IATHRQLSVLHPHKLVPHYKDTMFINASARQVLINANGLIETHYPSKYSMELSSILY 611  
Db 534 IATHRQLSVLHPHKLVPHYKDTMFINAMARQILINAGGVLESTVFPKFAVMSAVVY 593  
Qy 612 KDWTFPDQALPNNLMKRGAVEDSSAPHLRLINDYPAVDGLDITWSAKITWVODYCC 671  
Db 594 KDWTFPDQALPADLVKRGVAVEDSSSPHGKLLIEDIPYAVDGLIEIWSAKITWVODY 653  
Qy 672 YYKDDNAVQDFLOSWMNELREKGHADKKEHPMPKXQMTLSIELIBSCTTIIWIASALHA 731  
Db 654 YXGSDEELKDNELQAWNKELREVGCHGDKNEPMPWEVETPQELIDSCITIIWIASALHA 713  
Qy 732 AVNFGQVPGYILNRPPTTSRFRMPEVGTAEYKELESNPKAFRTICSELOALVSIISII 791  
Db 714 AVNFGQVPGYILNRPPTTSRFRMPEVGTAEYKELESNPKAFRTICSELOALVSIISII 773



```
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR OXidoreductase.
SQ SEQUENCE 862 AA; 97778 MW; 946679AF56041E89 CRC64;

Query Match
Best Local Similarity 63.1%; Score 2948.5; DB 10; Length 862;
Matches 534; Conservative 138; Mismatches 168; Indels 5; Gaps 3;

QY 39 GNKIKGKVMKSNVLDPTFEHNSLNDFTFELGGVSPQLISATHT--SNDSRGKGVNK 96
DB 18 GKVKGTIVLMKKVLDNDVNASLDDGVLEFLGKRVSLQLISVHADPGNSLQKSNP 77
QY 97 AYLERWLTSIPPLFAGESVQINFOWDENFGPPGAFKNGHTSEFFLKSLTLDVPGY 156
DB 78 AYLERKWLTTGTSVAGESAFDFTDDEIDGVGAFIINNFHNEFYLSLTLEDVPHG 137
QY 157 RVHFDNSWVPSGRYKDKRIFFANHVLPSTQENPLKRYEELWNLRGDGTGERKWD 216
DB 138 NVHFCVNSWVPAKYKSERIFFANQAYLPGETPEPLRYREKELNLRGNGKLBWD 197
QY 217 RIYDVYNDIADDPVGDH--RPILGGTTEYPYPRRGTRPRRRDHNYSRLSPMSL 274
DB 198 RYDYALYNDLGDPEKQYARTILGSAEYYPARGRTGKPKADPKSESRIPLMSL 257
QY 275 DIYVKDENFGLKMSDFLYTKALSISIKPGLOSIFDVTPNFDNFKVDNLFERGF 334
DB 256 DIYVPRDRFGRHKLSDFTLTKLSIVQFLIPEFOALFDSFTDFDSEFVLYKYE 317
QY 335 IPFNAF-KTLTDELTTPPLFKALVRNDGKFKLFTPEVVKDKNGKWSDFEFAREMLAGP 393
DB 318 LPQGFELKALTDISILETLKEIIRTDGSGKFKFTPPQVIQEDKSWRTDEFAREMLAGV 377
QY 394 NPLIRLRLEAPPTSKLPDNYGNQNSTITBEHKGHLGDLGTVDAMKQNELYIVDFHA 453
DB 378 NPVILSRLOEFPKPSQLDSEYVGNQNSTITKEHIENTUDGLTIDDAIKTNRLYILNHHDI 437
QY 454 LMPYLTRNATSTKYATRTLLKDDGTPLKPLVIELALPHQDGLGALSKLYFPAENG 513
DB 438 LMPYVRINTNTKLYASRTLLFLQDDGTMPVAIELSLPHDGDGLGAVSKVTPADQG 497
QY 514 VQKSIWQLAKAYVTVNDVGVHQLISHMLHHTHAVLEPPVIAHTRQLSVLHPHKLIVPHYK 573
DB 498 VEGSIWQLAKAYVAVNDSGVHQLISHMLNTHAATEPFIATNRQLSVLHPHKLHHPFR 557
QY 574 DTMFINASAROVLINANGLIETHYPSKYSNELSILYKDWTFPDQALPNNLMKRGAVE 633
DB 558 DTMNINAROLLINAGVLEWTFPPAKYAMSAVYKSVWVFPEQALPADLIRGVAVE 617
QY 634 DSSAPHGLRLINDYPFVADGLDWSAIKTWVQVCCLYYKDDNAVONDFELQSWNNELR 693
DB 618 DSSPHGVLLIQDYPYAVDGLIWSAISKSVTEYCNFYKSDLVKDNELQAWKELR 677
QY 694 EKHADKKEHPWPKMQLSLIESCTIIIMASALHAANFGQYPCGGIILNRPPTSRR 753
DB 678 BEGHDKKDEPWPMPQTRQKSDCTIIIMASALHAANFGQYPCGGIILNRPPTSRR 737
QY 754 FMPEVGTAEYKELESNPEKAFRLTICSLQALVSIISITELSKHASDEVYLGQASIDWT 813
DB 738 FMPEPGTPEYBELKTNPKAYLKITPQLQTLIGLSIELISRHASDEIYLGQDSSEWT 797
QY 814 SDKIALEAFKPKMFLFVENRIMERNKENVLNKRSQVNLPTVLLVPSNEGTLGRGIP 873
DB 798 KDQEPFAAFERFKKLSIEDQIIQMNGDKKWKNSRSPVNVPTLLPFTSEQGLTGKIP 857
QY 874 NSISI 878
DB 858 NSVSI 862

Query Match
Best Local Similarity 63.0%; Score 2946; DB 10; Length 862;
Matches 541; Conservative 138; Mismatches 170; Indels 8; Gaps 7;

QY 30 ILDRVSSL-GGNKIKGKVMKSNVLDPTFEHNSLNDFTFELGGVSPQLIS-ATHTSN 87
DB 6 IVDSITGDKDGEKVKGTIVLMKKVLDFTDVTASIVDGALEFLGRRVSPQLISNVHDAN 65
QY 88 DSRGKVCNKAYLERWLTSIPPLFAGESVQINFOWDEN-FGPPGAFKNGHTSEFFLKS 146
DB 66 GLEGKLSNPAYLENITNITPVVAGESTFSVTFDWDDEFGVPGAFIINKLHFSEFFLKS 125
QY 147 LTLDVDPGGRVHFDNSWVPSGRYKDKRIFFANHVLPSTQENPLKRYEELWNLRG 206
DB 126 LTLHEVFNHGKVFHVCNSWVYPSKYSKSDRIFFANQAYLPSETPELLKRYENELVALRG 185
QY 207 DGTGERKWDRIYDVYNDIADDPVGDH--RPILGGTTEYPYPRRGTRPRRRDHN 264
DB 186 DGTGLEEDRVYDYAVYNDLGDPEKQYARTILGSAEYYPARGRTGKPKADPKSESRIPLMSL 245
QY 265 ESRLSPIMSLDIYVVDENFGLKMSDFLYTKALSISIKPGLOSIFDVTPNFDNFKVDN 324
DB 246 ESRIPLMSLDIYVPRDRFGRHKLSDFTLTKALSISQLLDEFKALFDSFTNEFDSPAD 305
QY 325 VDNLFERGFPIPN-AFKLTLEDLTPPLFKALVRNDGKFKLFTPEVVKDKNGKWSDFE 383
DB 306 VLKIVEGGIKLPOGLPKFAIVDAIPLLETLKQLLSTDEGELLKYPPTQVIOEDKSAWRTDE 365
QY 384 EFAREMLAGPNLIRLRLEAPPTSKLPDNYGNQNSTITBEHKGHLGDLGTVDAMKQ 443
DB 366 EFGREMLAGINPVILSRLOEFPKPSQLDSEYVGNQNSTITKEHIENTUDGLTIDDAIKTN 425
QY 444 RLVIYDFHDALMPYLTRMN-ATSTKYATRTLLKDDGTPLKPLVIELALPHQDGLG 502
```

```
Db 426 RLFLINHHDIIMPVYRRINTTNTKMATRLLFLQDDGTLKPLAIELSLPHPDGDFGA 485
Qy 503 ISKLYFPAENGQKSIWOLAKAYTVNDVGVHQLISHWLHTHAVLEPFIATHRQLSVLH 562
Db 486 VSEVFTPSDQGVESIWOLAKAYAAVNDVGVHQLVSHWLNTHVIEPFIATNRQLSVLH 545
Qy 563 PIHKLVLPHYKDTWPFINASROVLINANGLIETHTHYSKYSMELSSILYKDWTFPPDALP 622
Db 546 PIHKLVLPHFRDTWMINALAQILNGGLLELTVFPKYSMELSSVYIKDWTFPEQALP 605
Qy 623 NNLKMRGLAVDSAPHGRLLLINDYPPAVDGLDIWSAIIKTWODYCCLYYKDDNAVQND 682
Db 606 ADLIRKGVAVDSNSPHGVRLLIODYPYAVDGLSIWSAIIKSWTEYCNYYKSDDAVQKD 665
Qy 683 FELOSNNELREKGHADKKHPPWPKMOTLSIELSCCTIWIASALHAANVFGQYPYGG 742
Db 666 AELQAWKELREEGHDKKDBPWPQMOSVQELIDSCITITIIASALHAANVFGQYPYAG 725
Qy 743 YILARPPTSRPMPRVGTAEYKELESNEPEKAFLETICSELOALVSIISIILSKHASDEV 802
Db 726 YLNPPTTSRPMPPBPGAEYELKRNDPNVFLKTIIPQLOTLVGISIELLSHSDTL 785
Qy 803 YILGRASIDWTSKIALBAFEGKGNLPEVENRIMERKE-VNLKNSRGPVNLPTLLVP 861
Db 786 YLGQDSPEWTKQBPISAFERFGKLGIEIDRIIQMGNDKQKNSRGPVNVPTLLFP 845
Qy 862 SSNEGLTGRIIPNSISI 878
Db 846 TSEGLTGKIPNSVSI 862

RESULT 10
Q9LEA9 PRELIMINARY; PRT; 862 AA.
ID Q9LEA9
AC Q9LEA9
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OC NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=sv. Scorza verde;
RX MEDLINE=21153257; PubMed=11231304;
RA Mita G., Gallo A., Greco V., Zasiura C., Casey R., Zacheo G.,
RA Santino A.;
RT "Molecular cloning and biochemical characterization of a lipoxigenase
RT in almond (Prunus dulcis) seed.";
RL Eur. J. Biochem. 268:1500-1507(2001).
RR EMBL; AJ404331; CAB94852.1; -.
DR HSP; P08170; 2SB.
DR GO; GO:0005506; P:iron ion binding; IEA.
DR GO; GO:0016165; P:lipoxigenase activity; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR01024; Lipoxigenase_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PRO0087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Oxidoreductase.
SEQUENCE 862 AA; 980:9 MW; EE078F795F435626 CRC64;
```

```
Query Match 62.9%; Score 2942.5; DB 10; Length 862;
Best Local Similarity 62.2%; Pred. No. 2.5e-211;
Matches 534; Conservative 143; Mismatches 173; Indels 9; Gaps 3;

Qy 29 NTLDRVSSLGNN-----KIKGVILMRSNVLDFTEFHNLLDNFTLGGGVSPQLISAT 83
Db 4 NLFDKITGOEQNGKNSRKIKGVILMKXNVLDNFDFNASVLDLRVHELLGQGVSLQLISAD 63
Qy 84 H--TNSDRGRKGVNKAYLERMLTSPPLPAGESVFPQNFQWDENFPGFCARFIKNHGTSE 141
Db 64 HGDSENGFKGLGEPAYLEDWITTTPLTIGDSAYKVTDFWEEIEIGVPCAILIKNNHSE 123
Qy 142 FFLKSLTLDVDPGYGRVHFDCNSWYPSGRYKDKRIFFANHVLYPSQPNLPKRYREBEL 201
Db 124 FFLKTIITLDEVPRGRVHFVCSWYPAEKT'KURVFFVNTFPLPSETPLPARKYREBEL 183
Qy 202 WNLRGDGTGERKEWDRIYDYVDYNDIADPDVGDH--RPILGTTETYPYPRGRTGRPSR 259
Db 184 VHLRGDGKGLQEDVRVYDAYYNDLGNPDKPKYARPTLGGSSSEYPYPRGRTGRPPTK 243
Qy 260 RHNYESRLSPIMSLDIYVPKDNFENFGLKMGDFGLYTLKALSISIKPGLSIEDVTPNEF 319
Db 244 TDSNESRIPPLMSLNIYVPRDERFGHLKLSDFLAYALKSIVQFIRPELEALFKTPNEF 303
Qy 320 DNFKVDNLFERGFPIPFNAFKTLTDELTPPLFKALVRNDGEEKFLKFTPTPEYKDKNIGW 379
Db 304 DSLEDVLKLYGGIPLPESGLLKIDGNIPAEMLKEIFRTDGAQLLRFPMPOVIEBKSAM 363
Qy 380 STDEPFAREMLAGNPILLIRLEAPPTSKLDPNVYQNQNTIIEEHKKGDLGLTVDEA 439
Db 364 RTDEPFAREMLAGVNPVNISLQEPFPASKLDPKVGQDTSRTIQDIGNKLDGLTVHEA 423
Qy 440 MKONRLYIVDFHDALMPYLTRMNATSTKYATRTLLLLKDDCTLKPVLIELALHPQDQ 499
Db 424 LKONKLFILHHDALMPYLRLINSTNKIYASRTVLFLKSDGTLKPLVIELSLPHPDGQ 483
Qy 500 LGAISKLYPFAENGQKSIWOLAKAYTVNDVGVHQLISHWLHTHAVLEPFIATHRQLS 559
Db 484 FGRISKVYTPABEGVEGSIWOLAKAYVAVNDVGVHQLISHWLNTHAVCEPVIATNRQLS 543
Qy 620 ALPNMLKREGLAVDSAPHGRLLLINDYPPAVDGLDIWSAIIKTWODYCCLYYKDDNAV 679
Db 604 ALPADLINRGVAVKDANSPHGRLLLIDDPYAVDGLSIWFAIKTWVEDYCSFYKTDII 663
Qy 680 QNDFELQSWNELREKGHADKKHPPWPKMOTLSIELSCCTIWIASALHAANVFGQYP 739
Db 664 QNDIELQSWNELREKGHADKKHPPWPKMOTLSIELSCCTIWIASALHAANVFGQYP 723
Qy 740 YGYIINRPTTSRRRPMPEVGTAEYKELESNEPEKAFLETICSELOALVSIISIILSKHAS 799
Db 724 YAGYLPNRPTISRKFMPEKGTPEYKELESSEPDVFLKTIITAOQLTVGLIALIELLSRST 783
Qy 800 DEVYLQORASIDWTSKIALBAFEGKGNLPEVENRIMERKEVNLKNSRGPVNLPTLL 859
Db 784 DEVYLQORDTPPTWATDTEPLKAFKFGSKLAIEDRIITRMNDEKLKORVGPVKPYTLL 843
Qy 860 VPSNNEGLTGRIIPNSISI 878
Db 844 PFTSEGLTGRIIPNSVSI 862

RESULT 11
Q9LEA9 PRELIMINARY; PRT; 861 AA.
ID Q9LEA9
AC Q9LEA9
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
```

DE Lipoxigenase (EC 1.13.11.12).  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tuber;  
RX MEDLINE=96355454; PubMed=8702864;  
RA Rojo J.N., Vancanney G., Perez A.G., Sanz C., Stormann K., Rosahl S.,  
RA Sanchez-Serrano J.J.;  
RT "Characterization of three potato lipoxigenases with distinct  
RT enzymatic activities and different organ-specific and wound-regulated  
RT expression patterns.";  
RL J. Biol. Chem. 271:21012-21019(1996).  
RL EMBL; X95513; CAA64766.1; -;  
DR HSSP; P08170; 28BL.  
DR GO; GO:0005506; F:iron ion binding; IEA.  
DR GO; GO:0016185; F:lipoxigenase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR000907; Lipoxigenase.  
DR InterPro; IPR01024; Lipoxigenase\_LH2.  
DR Pfam; PF00305; lipoxigenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS00095; PLAT; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 861 AA; 97067 MW; 25783F32C698FA26 CRC64;

Query Match 62.9%; Score 2941; DB 10; Length 861;  
Best Local Similarity 64.6%; Pred. No. 3.2e-211;  
Matches 545; Conservative 118; Mismatches 175; Indels 6; Gaps 4;

QY 41 KIKGKVLMSNVLDFTFHNLDNFTTELLGGVSTFOLISATH--TSNDRGRKVGKAY 98  
DB 18 KLGTVVMNKNALDFTDLGSLTKAFELGQTVSFQSLISSVQGDPTNGLOKHSNPA 77  
QY 99 LERWLTSTPLPAG-ESVFQNFQWENFPGPAFFIKNGHTSEFFLKSITLDDVPYGR 157  
DB 78 LENSFLTLPTAGSETAFGTFPWNHEFGVGFAGFIKXTHINEFFLKSITLDDVPNHGK 137  
QY 158 VHFQNSWVPSGRYKXDRIFFAHNVLPQTPNPLRYREBELNLRGDTGERKEWDR 217  
DB 138 VHFVNSWVPSRYKSDRIFPFVQNPYLPSTPELLRKYRENEILLTRGGDTGKREAWDR 197  
QY 218 IYDYVDNDIADPDVGDH--RPILGGTTEYPYPRGRGTGRPRSDHNYESRLSPMSLD 275  
DB 198 IYDYDINDLGNDEGENKNTLGGSAEYPYPRGRGTGRPTTDPKSESRIPLILSLD 257  
QY 276 IYVPKDNFGLKYSDFLYTKALSISIKPGLQSIQFDPVTFNPFKEVDNLFERGFPI 335  
DB 258 IYVPRDERFGLKWSDFLYTKALSIVQFIPLPALFDGTPNEFDSPEVDLRYEGGKL 317  
QY 336 PFN-AFKTLTLEDLPPELKAIVRNDGKFLKFPFTEVVKNNKIGWSDEFEAREMLAGPN 394  
DB 318 PGGFLFKALTAAPLEMIREULRTDGGIURFPPLVVKDKSTAWRTDEFEAREMLAGVN 377  
QY 395 PLLRRLEAFPTSKLPDNPVGNQNSITTEHIXKHGDLGTLTVDEAMQNQLYIVDFHDAL 454  
DB 378 PVILSRLOEFPKSKLDEAGNQNSITTAHIEDKLDGLTVDEAMNNKLFILNHHIDL 437  
QY 455 MPYTRMNTATKTYATRTLLLLKDDGTLKPLVTELALPHQGGOLGAISKLFPBAENG 514  
DB 438 IPYLRINNTTKTYASTLLFLQDNGSLKPLAELSLPHPDGQFGVTSKVTPSDQGV 497  
QY 515 QKSIWOLAKAYVYNDVGYHOLISHWLTHAVLEPFIATHRQLSVLHPHKLAVPHYKD 574

DB 498 ESSIWQLAKAYVAVNDSGVHQLISHWLNTHAVIEPFIATNRQLSVLHPHKLPHFRD 557  
QY 575 TWFINASQVLINANGLIETHYPSKYSMELSSILYKDWTFPDQALPNMLMKRGAYED 634  
DB 558 TWNIAMARQILINAGVLESIVFQSKFAMENASVYKDWTFPDQALPADLYKRGVAVED 617  
QY 635 SSAPHLRLRLINDYPFVAVDGLDWSAIKTWQDYCCLYYKDDNAVQNDPFLQSMWNLRE 694  
DB 618 SSSPHGVRLIEDYPFVAVDGLDWSAISKWSVSDYCSFYGSDDEILKNELQAMWKLRE 677  
QY 695 KGHAKKHPKPKMOTLSIELSCCTTIWTASALHRAVNEGOYPGVILNRPVTSRRF 754  
DB 678 VGHGDKKNEPWPMEWEPQELIDSCCTTIWTASALHRAVNEGOYPGVILNRPVTSRRF 737  
QY 755 MPEVGTAEYKELESNEPEKAFRTICSELQALVSIISILSKHAGDEYVLQGRASIDWTS 814  
DB 738 MPEPGTPEVEELKKNPDRAFLTKITTAQLQTLGVSLEILSRHTTDEIVLGQRESPEWTK 797  
QY 815 DKIALEAPEKFKGNLFEVENRIMERKENVLNKRGSPVNLPTLLVSPNSGLTGRIPLN 874  
DB 798 DKEPLAFAFDKFGKLTDEKQIQRNGNLTNRSGPVNAPYVTLTFTSEGLTGKIPN 857  
QY 875 SISI 878  
DB 858 SVSI 861

RESULT 12  
O22508 PRELIMINARY; PRT; 861 AA.  
AC O22508;  
DT 01-JAN-1998 (TREMELrel. 05, Created)  
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Lipoxigenase.  
GN PLOX2.  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Lehmi Russet; TISSUE=Tuber;  
RA Fidansef A.L., Bostock R.M.;  
RT "Solanum tuberosum (Lehmi Russet) lipoxigenase (plox2) mRNA, complete cds.";  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF019614; AAB81595.1; -;  
DR HSSP; P09186; 1LNH.  
DR GO; GO:0005506; F:iron ion binding; IEA.  
DR GO; GO:0016185; F:lipoxigenase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR000907; Lipoxigenase.  
DR InterPro; IPR001024; Lipoxigenase\_LH2.  
DR Pfam; PF00305; lipoxigenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS00095; PLAT; 1.  
SQ SEQUENCE 861 AA; 97020 MW; 92C31F6EAF55PB58 CRC64;

Query Match 62.9%; Score 2939; DB 10; Length 861;  
Best Local Similarity 63.9%; Pred. No. 4.5e-211;  
Matches 544; Conservative 124; Mismatches 173; Indels 10; Gaps 5;

QY 38 GGN----KIKGKVLMSNVLDFTFHNLDNFTTELLGGVSTFOLISATH--TSNDRGR 91  
DB 11 GGHDDSKVKGVVVMNKNVLDFTDLASSLTGKIFDLVGLQKVSFOLISSVQGDPTNG 70

```
QY 92 KVGKAYLERLWTSIPPLFAG-ESVQINFWNDENFGPGAFFIKNGHTSEFFLKSITLD 150
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 KHSNPAYLENSLFTLTPLTAGSETAFGVTFDWNEFGVPGAFIKNWHIEFFLKSITLE 130
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 151 DVPGRVHPCNSWVPSGKDYKDRIFFAHNVLPQOTPNPLKYEELWNRGDGTG 210
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 DVPNHGKHVFCNSWVPSLNYKSDRIFFANQYLPSETPELLKRYENELLTURGDTG 190
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 211 ERKENDRIYDVNDIADDPVGDH--RPILGGTTEYPYPRGRGTGRPRGRDHNYSRL 268
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 KREANDRIYDYIYNDLGNPQKGNVTTLGGSAEYFPYPRGRGTGPTTTPKVKSR 250
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 269 SPIMSLDIYVKDENFGLKMSDFLGYTLKALSISIKPGLOSIFDVTNFDNFKVDNL 328
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 251 PLILSLDIYVPRDERFGLKMSDFLTKALSIKIVFILPELHALPDGTNFDNFKVDNL 310
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 329 FERGGPIPFN-AFKLTLEDLTPPLFKALVRNDGKFLKFPPEVVKDKNGKWSDEBFAR 387
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 311 YEGGKLPQGLPKALTAIAPIEMIRELLRTDGEILRFPPLVVKSKTAWRTDEBFAR 370
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 388 EMLAGNPILLIRLEAFPTTSKLDPNVYGNQNSTITEHKGHLDGLTVDAMKQNLRY 447
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 371 EMLAGNPILLIRLEAFPTTSKLDPNVYGNQNSTITEHKGHLDGLTVDAMKQNLRY 430
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 448 VDFHDMALPYLTKMNTATSTKYATRTLLKDDGTLKPLVIELALPHPQDGLGALS 507
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 431 LNHHDVIIPIYLRRIINTITTKTYAGRTLLFLQDNGSLKPLALELSPHDPDGTG 490
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 508 FPAENGVSQSIWQLAKAYVTVDVGYHQLISHWLTHAVLEPFIATHRQLSVLHPHKL 567
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 491 TPDQGVSESSIPHGVLLIEDYFYAVDGLGELWALSIAKSWVTDYCSFYGSDEILK 670
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 688 WNEIREKHADKHGHPWPKMQLSELIESCTTIWIASALHAANFGQYPGGYTLNR 747
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 671 WNKELREVGHDGKNEPWPMPKTPQELIDSCCTTIWIASALHAANFGQYPGGYTLNR 730
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 748 PTTGRRFPEVGTAEYKELESNPKAFRTTICSELOALVSTISITELSKHASDEVYLG 807
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 731 PTVSERFNPFGTPEYELKKNPKAFKTTITAOQLTGLGSLVELLSRHTTDEIVLGR 790
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 808 ASIDWTSKIALEAFEPKGNLFEVNRIMERNEKVNLRSGPVNLPYTLVPSNNEGL 867
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 791 ESPEWTCKEPLAADFREGKLTIDIEKQIIQRNGDNILNRSQGVNAPYTLVPSNNEGL 850
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 868 TGRGIPNSISI 878
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 851 TKGIPNSVSI 861
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
Q9SC16 PRELIMINARY; PRT; 861 AA.
AC Q9SC16
DI 01-MAY-2000 (TRENBLrel. 13, Created)
DI 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DI 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX1-ST-2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=cv. Desiree; TISSUE=Tuber;
RX MEDLINE=21066065; PubMed=11139400;
RA Hughes R.K., West S.I., Hornostaj A.R., Lawson D.M., Fairhurst S.A.,
RA Sanchez R.O., Hough P., Robinson B.H., Casey R.;
RT "Probing a novel potato lipoxigenase with dual positional specificity
RT reveals primary determinants of substrate binding and requirements for
RT a surface hydrophobic loop and has implications for the role of
RT lipoxigenases in tubers.";
RL Biochem. J. 353:345-355(2001).
DR EMBL; Y18548; CAB65460.1; -.
DR HSSP; P09186; 1LNX.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Oxidoreductase.
SQ SEQUENCE 861 AA; 96964 MW; 653ED518108BDFDC CRC64;

Query Match 62.8%; Score 2936; DB 10; Length 861;
Best Local Similarity 63.8%; Pred. No. 7.5e-211;
Matches 543; Conservative 125; Mismatches 173; Indels 10; Gaps 5;

QY 38 GGN----KIKGVILMRSNVLDTTEFHSNLLDNTELLGGVSGQLISATH--TSNDSRG 91
Db 11 GGHDSKVKVGTVMNKNVLDFTDLAGSLTKGIFDVLGQKVSQQLISSVGDPNGLQG 70
QY 92 KVGKAYLERLWTSIPPLFAG-ESVQINFWNDENFGPGAFFIKNGHTSEFFLKSITLD 150
Db 71 KHSNPAYLENSLFTLTPLTAGSETAFGVTFDWNEFGVPGAFIKNWHIEFFLKSITLE 130
QY 151 DVPGRVHPCNSWVPSGKDYKDRIFFAHNVLPQOTPNPLKYEELWNRGDGTG 210
Db 131 DVPNHGKHVFCNSWVPSLNYKSDRIFFANQYLPSETPELLKRYENELLTURGDTG 190
QY 211 ERKENDRIYDVNDIADDPVGDH--RPILGGTTEYPYPRGRGTGRPRGRDHNYSRL 268
Db 191 KREANDRIYDYIYNDLGNPQKGNVTTLGGSAEYFPYPRGRGTGPTTTPKVKESRI 250
QY 269 SPIMSLDIYVKDENFGLKMSDFLGYTLKALSISIKPGLOSIFDVTNFDNFKVDNL 328
Db 251 PLILSLDIYVPRDERFGLKMSDFLTKALSIKIVFILPELHALPDGTNFDNFKVDNL 310
QY 329 FERGGPIPFN-AFKLTLEDLTPPLFKALVRNDGKFLKFPPEVVKDKNGKWSDEBFAR 387
Db 311 YEGGKLPQGLPKALTAIAPIEMIRELLRTDGEILRFPPLVVKSKTAWRTDEBFAR 370
QY 388 EMLAGNPILLIRLEAFPTTSKLDPNVYGNQNSTITEHKGHLDGLTVDAMKQNLRY 447
Db 371 EMLAGNPILLIRLEAFPTTSKLDPNVYGNQNSTITEHKGHLDGLTVDAMKQNLRY 430
QY 448 VDFHDMALPYLTKMNTATSTKYATRTLLKDDGTLKPLVIELALPHPQDGLGALS 507
Db 431 LNHHDVIIPIYLRRIINTITTKTYAGRTLLFLQDNGSLKPLALELSPHDPDGTG 490
QY 508 FPAENGVSQSIWQLAKAYVTVDVGYHQLISHWLTHAVLEPFIATHRQLSVLHPHKL 567
Db 491 TPDQGVSESSIPHGVLLIEDYFYAVDGLGELWALSIAKSWVTDYCSFYGSDEILK 550
QY 568 LVPYKDTMFINASARQVLINANGLIETHYPSKYSELSSILYKDWTFDQALPNMLK 627
Db 551 LYPHFRDTMFINASARQVLINANGLIETHYPSKYSELSSILYKDWTFDQALPNMLK 610
QY 628 RGLAVEDSSAPHGLRLINDYFFAVDGLDIWSAKITWQDYCCLYYKDDNAVNDFELQS 687
```

```

Db 611 RGAVEDSSPHGVRLIEDYPAVADGLEIWSAIAKSWTDCFYGSDDEILKDELQA 670
Qy 688 WNNELREKGHADKHHEPWPQWOTLSLIESCTIIWIASALHAANFGOPYGGVILNR 747
Db 671 WVKELREVGCHDKXNEPWFEMKTPQELIDSCITIIWIASALHAANFGOPYAGVILPNR 730
Qy 748 PTTSSRRFMPVGTAEYKELESNPEKAFRTICSELQALVSIISIEILSKHASDEVYLGQR 807
Db 731 PTVSSRRFMPVGTAEYKELESNPEKAFRTICSELQALVSIISIEILSKHASDEVYLGQR 790
Qy 808 ASIDWTSKDALEAFEFKGNLFVEVNRIMERKNVKNRSGPVNLPYTLIYVSSNEGL 867
Db 791 ESPSWTKDKEPLAADFPGKLLDIEKQIIQRNGDNILTRNSGVNAPYTLIYVSSNEGL 850
Qy 868 TGRGIPNSISI 878
Db 851 TGKGIPIVSVSI 861

RESULT 14
Q8W4X6
ID Q8W4X6 PRELIMINARY; PRT; 862 AA.
AC Q8W4X6;
DT 01-MAR-2002 (TremBrel. 20, Created)
DT 01-MAR-2002 (TremBrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN Lox.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_taxid=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Scorza verde;
RA Mita G., Gallo A., Fasano P., Zasilura C., Casey R., Santino A.;
RT "Molecular cloning of an almond lipoxigenase gene expressed during the
RT early stages of seed development.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ418043; CAD10779.2; -.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR KX Oxidoreductase.
SQ SEQUENCE 862 AA; 97751 MW; 3FAC9D205DCBC131 CRC64;

Query Match 62.7%; Score 2931.5; DB 10; Length 862;
Best Local Similarity 61.9%; Pred. No. 1.6e-210;
Matches 532; Conservative 144; Mismatches 174; Indels 9; Gaps 3;

Qy 29 NILDRV-----SSLGKNGKIKGVILMRSNVLDFTEPHSNLLDNFTLLGGGVFQILSAT 83
Db 4 NLFDKITQEQNGKNGKIKGVILMRKNVLDNFDFNASVLDVDRVHLLGGVSLQLISAD 63
Qy 84 H--TSNDSRGKGNKAVLERWLTSIPPLFAGESVQINFDNENFGPPGAFFTKNGHSE 141
Db 64 HGDSNGFKGKGLGPAYLEDWITITPLTVGDSAYNVTFDWEIEIGVFGAILKNNHSE 123
Qy 142 PFLKSLTLDVPGVGRVHFCNCSWVPSGRYKDKRIFFANHVLPSTPNPLKRYEEL 201

```

```

Db 124 PFLKTVTLIEDVPREGRVHFVCNWSVYPAEKYTKORVFFVNKTFLPSETPLPLRKYREBEL 183
Qy 202 WNLRGDGTGERKEWDRIYDYVDYNDIADPDYGDH--RPILGGTTEYPVPRGRGTRPSRSR 259
Db 184 VHLRGDGGELQEWDRVYDAYYNDLGNPDGSKYARPTLGGSSGYPPPPRGTRPATK 243
Qy 260 RDHYESRLSPIMSLDIYVPKDNFPHLKMDSDFLGYTLKALSISIKPGLQSFIDVTPNEF 319
Db 244 TDPNSESRIPLIMSLNVVPRDERFHLKLSDFLAYALKSIVQFIRPELEALFDPKTFNEF 303
Qy 320 DNFKVDNLPFERGFPIFENAKTLTEDLTPPLFALVENDGKELKPTPEVVDXNKIGW 379
Db 304 DSEFVLLKLYTGGIPLPEGLLKIDIGNIPAEMLEIFFTDGAQLLRFPMPOVIEEDKSAW 363
Qy 380 STDEFAFARMLAGNPILLIRLEAPPPSTKLDPNVYGNQNSTIITEEHIKHGLDGLTVDEA 439
Db 364 RTDEFAFARMLAGVNPVNISLLQEPFPASKLPNVYGDQTSRITTEQDIGNKLDGLTVHEA 423
Qy 440 MKQNELIYVDFHDALMPYLTRMNATSTKYATRILLLLKDDGTLKPLVIELALPHPDQDQ 499
Db 424 LKQNKLFILDHHDALMPYLRRINSTSNKIYASRTVFLKSDGTLKPLVIELSLPHPDQDQ 483
Qy 500 LGAIKSLYFPAENGVOKSIWOLAKAYVTVDVGVHQLISHWLHTHAVLEPFVIATHROLS 559
Db 484 FGRISKVYTPAEEGVEGSIWOLAKAYVAVNDGSHQLISHWLHTHAVCEPVVIATNROLS 543
Qy 560 VLHPHKLILVHYKDTMFINASAROVLINANGLIETTHYPSKYSMELSSILYKOWTFPDQ 619
Db 544 VVHPYIKLHHPHFRDTMFINAFARQIVINAGGILETTVPFSRYAMELSSVYKOWVTFEQ 603
Qy 620 ALPNNLMKRGGLAVEDSSAPHGLRLILINDYPPAVDGLDIWSAIAKSWTDCFYGSDDEILKDELQA 679
Db 604 ALPADIILKRGVAVKANSFPHGLRLILIEDYPYAVDGLDIWFAIKWVEDYCFYKTDITII 663
Qy 680 QNDFELQSWWNLREKHGADKHHEPWPQWOTLSLIESCTIIWIASALHAANFGOPY 739
Db 664 QSDTELQSWWNLREKHGADKHHEPWPQWOTLSLIESCTIIWIASALHAANFGOPY 723
Qy 740 YGGYILNRPPTSSRRFMPVGTAEYKELESNPEKAFRTICSELQALVSIISIEILSKHAS 799
Db 724 YAGYLPNRPPTSSRRFMPVGTAEYKELESNPEKAFRTICSELQALVSIISIEILSKHAS 783
Qy 800 DEVILGQRASIDWTSKDALEAFEFKGNLFVEVNRIMERKNVKNRSGPVNLPYTLI 859
Db 784 DEVILGQRDTEWTDATPEPLKAFKFKGLAKIEDRITSMNDEKLNKRVGVKVPYTLI 843
Qy 860 VPSSNEGLTGRGIPNSISI 878
Db 844 FPTSGGLTGRGIPNSVSI 862

RESULT 15
O22507
ID O22507 PRELIMINARY; PRT; 861 AA.
AC O22507;
DT 01-JAN-1998 (TremBrel. 05, Created)
DT 01-JAN-1998 (TremBrel. 05, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Lipoxigenase.
GN FLOX1.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=41113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lehmi Russet; TISSUE=Tuber;
RA Fidanseef A.L., Boscock R.M.;
RT "Solanum tuberosum (Lehmi Russet) lipoxigenase (plox1) mRNA, complete
RT cds.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF019613; AAB81594.1; -.

```





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2004, 12:03:09 ; Search time 139.206 Seconds  
(without alignments)

1971.379 Million cell updates/sec

Title: US-09-937-908-1

Perfect score: 4675

Sequence: 1 MFGIGKNIIEGALNTGDLA.....LVPSNGLTGRGIPNSISI 878

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1285345 seqs, 31250633 residues

Total number of hits satisfying chosen parameters: 1285345

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	3933	84.1	US-10-059-909-12	Sequence 12, Appl
2	3011.5	64.4	US-09-978-522-3	Sequence 3, Appl
3	2995.5	64.1	US-09-978-522-1	Sequence 1, Appl
4	2929	62.7	US-10-425-114-54449	Sequence 54449, A
5	2795	59.8	US-10-424-599-215976	Sequence 215976, A
6	2795	59.8	US-10-425-114-45769	Sequence 45769, A
7	2795	59.8	US-10-425-114-54429	Sequence 54429, A
8	2795	59.8	US-10-425-114-55253	Sequence 55253, A
9	2791	59.7	US-09-751-687-17	Sequence 17, Appl
10	2742.5	58.7	US-10-424-599-215973	Sequence 215973, A
11	2742.5	58.7	US-10-425-114-45631	Sequence 45631, A
12	2713.5	58.0	US-10-425-114-46828	Sequence 46828, A
13	2706.5	57.9	US-10-424-599-220216	Sequence 220216, A
14	2700.5	57.8	US-10-424-599-239573	Sequence 239573, A
15	2690	57.5	US-10-424-599-213159	Sequence 213159, A

16	2690	57.5	US-09-751-687-16	Sequence 16, Appl
17	2656.5	56.8	US-10-424-599-258944	Sequence 258944, A
18	2655.5	56.8	US-10-425-114-42385	Sequence 42385, A
19	2653	56.7	US-10-424-599-161981	Sequence 162981, A
20	2653	56.7	US-10-425-114-57755	Sequence 57755, A
21	2653	56.7	US-10-425-114-45728	Sequence 45728, A
22	2653	56.7	US-10-425-114-62362	Sequence 62362, A
23	2644.5	56.6	US-10-424-599-237909	Sequence 237909, A
24	2644.5	56.6	US-10-424-599-151513	Sequence 151513, A
25	2628.5	56.2	US-10-424-599-151513	Sequence 45902, A
26	2628.5	56.2	US-10-425-114-45902	Sequence 72413, A
27	2628.5	56.2	US-10-425-114-42413	Sequence 46295, A
28	2618	56.0	US-10-425-114-46295	Sequence 151512, A
29	2608.5	55.8	US-10-424-599-151512	Sequence 151512, A
30	2606	55.7	US-10-424-599-242598	Sequence 242598, A
31	2606	55.7	US-10-425-114-57754	Sequence 57754, A
32	2606	55.7	US-10-425-114-56555	Sequence 54555, A
33	2599	55.6	US-10-424-599-151510	Sequence 151510, A
34	2599	55.6	US-10-425-114-39867	Sequence 39867, A
35	2599	55.6	US-10-425-114-42418	Sequence 42418, A
36	2599	55.6	US-10-425-114-39883	Sequence 39883, A
37	2599	55.6	US-10-425-114-47348	Sequence 47348, A
38	2599	55.6	US-10-425-114-40151	Sequence 40151, A
39	2599	55.6	US-10-425-114-40047	Sequence 40047, A
40	2599	55.6	US-10-425-114-39889	Sequence 39889, A
41	2582.5	55.2	US-09-751-687-15	Sequence 15, Appl
42	2577.5	55.1	US-10-424-599-151515	Sequence 151515, A
43	2576	55.1	US-10-425-114-57794	Sequence 57794, A
44	2538.5	54.3	US-10-437-963-165232	Sequence 165232, A
45	2525	54.0	US-10-437-963-141895	Sequence 141895, A

ALIGNMENTS

RESULT 1

US-10-059-909-12

; Sequence 12, Application US/10059909

; Publication No: US20030074693A1

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Edgar B.

; APPLICANT: Kinney, Anthony

; APPLICANT: Klein, Theodore

; APPLICANT: Lee, Jian Ming

; APPLICANT: Pearlstein, Richard

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Shen, Jennie

; APPLICANT: Thorpe, Cathy

; APPLICANT: Tingey, Scott

; APPLICANT: Weng, Zude

; TITLE OF INVENTION: Plant Lipoxigenases

; FILE REFERENCE: B01333 US CIP

; CURRENT APPLICATION NUMBER: US/10/059,909

; CURRENT FILING DATE: 2002-01-29

; PRIOR APPLICATION NUMBER: 09/501,422

; PRIOR FILING DATE: 2000-02-09

; PRIOR APPLICATION NUMBER: 60/119,597

; PRIOR FILING DATE: 1999-02-10

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 12

; LENGTH: 880

; TYPE: PRT

; ORGANISM: Momordica charantia

US-10-059-909-12

Query Match 84.1%; Score 3933; DB 14; Length 880;

Best Local Similarity 81.7%; Pred. No. 0;

Matches 719; Conservative 83; Mismatches 76; Indels 2; Gaps 1;

QY 1 MFGIGKNIIEGALNTGDLAGSVINAGGNILDRVSSLGKNIKGKVLNRSNVLDFTEFH 60

Db 1 MFGIGKNIIEGALNTGDLAGSVINAGGNIVGRVTNIGKNIKGKVLNRSNVLDFTEFH 60

```

QY 61 SNLLDNFTLLGGVSYFOLISATHSTNSDRGKVGKAYLERWLTSIPLPAGESVFOINF 120
DB 61 SSLLDGVTELLGGISLQISATHASNDNRGKVGKAFERWLTSVPLPAGESVFOINF 120
QY 121 QNDNFPGFAPFIKNGHTSEFFLKSLLTLDVPGYGRVHFDNCNSWVYPSGRYKDKRIFFA 180
DB 121 DWENFPGFAPFIKNGHTSEFFLKSLLTLDVPGYGRVHFDNCNSWVYPSGRYKDKRIFFA 180
QY 181 NHVYLPSTQPNLRYRREELNWLSDGTGERKEWDRIYDVYDNDIADPDVGH--RPI 238
DB 181 NHTCLPIDPDSLRKYREELNWLSDGTGERKEWDRIYDVYDNDIADPDVGH--RPI 240
QY 239 LGGTYEYPRGRGTRPRSRDRHNEYSRLSPINSLDIYVVKDENFGLKMSDFLGYTLK 298
DB 241 LGGSDQYYPYPRGRGTRPRSRDRHNEYSRLSPINSLDIYVVKDENFGLKMSDFLGYTLK 300
QY 299 ALSISIKPGLQSIQFVTENEFDNFKEVDNLPERGPIPFNAFKLTEDLTPLPKALVRN 358
DB 301 VLSTIQPLESIFDSTGEFDKFEVDNLFERGPPIPLNIFKNLTEDLAPPLPKAFURS 360
QY 359 DGEKTLKPTPVPVWKNKIGWSTDBEFAREMLAGNPLLIIRLEAFPPSTSKLDPNVYGNQ 418
DB 361 DGERFLKYPTPOVKNKIGWSTDBEFAREMLAGNPLLIIRLEAFPPSTSKLDPNVYGNQ 420
QY 419 NSTITEEHKGLDGLTVDEAMKQNRXYIVDPHDALMPYLTRMATSXTKTYATRTLLLK 478
DB 421 NSTITEEQIKGLDGLTVDEAMKQNRXYIVDPHDALMPYLTRMATSXTKTYATRTLLLK 480
QY 479 DGTTLKPLVIELALPHQDQOLGALSILYFPAENGVOKSIWOLAKAYVTVNDVGHOLIS 538
DB 481 DOSTLKPALIELSLPHQDQDEHGAISKLYFPAENGVOKSIWOLAKAYVTVNDVGHOLIS 540
QY 539 HMLTHAVLEPVIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLINANGLIETHY 598
DB 541 HMLTHAVLEPVIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLINANGLIETHY 600
QY 599 PSKYNESSLILYKDWTPDOALPNNLMKRGGLAVEDSSAPHLRLINDYPPAVDGLDIW 658
DB 601 PAKYAMEUSSYLYKDWTPDOALPNNLMKRGGLAVEDSSAPHLRLINDYPPAVDGLDIW 660
QY 659 SAIKTWVQDCCLYKDDNAVQNDPELQSWNNELREKGHADKXHPWPMQOTSELIES 718
DB 661 SAIKTWVQDCCLYKDDNAVQNDPELQSWNNELREKGHADKXHPWPMQOTSELIES 720
QY 719 CTTIITIASALHAANFGQYPCYGYILNRPPTSRPFMEVGTAEYKELESNPEKAFURTI 778
DB 721 CTTIITIASALHAANFGQYPCYGYILNRPPTSRPFMEVGTAEYKELESNPEKAFURTI 780
QY 779 CSEALQVLSIIEILSKHASDEVYLGORASIDWTSKIALEAFKFKGNLFVEVENRIME 838
DB 781 SSOIALLGLSIIIEILSKHASDEVYLGORASIDWTSKIALEAFKFKGNLFVEVENRIME 840
QY 839 RNKEVNLKNSGPNVLPYTLVPSSNEGTLGRGIPNSISI 878
DB 841 RNQDVNLKNRAGPVNMPYTLVPSSNEGTLGRGIPNSISI 880

```

## RESULT 2

```

US-09-978-522-3
; Sequence 3, Application US/09978522
; Publication No. US2003003627A1
; GENERAL INFORMATION:
; APPLICANT: Descenzo, Richard
; APPLICANT: Irelan, Nancy
; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera
; FILE REFERENCE: 29520/37890
; CURRENT APPLICATION NUMBER: US/09/978,522
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,220
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 3
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Vitis LOX 2
US-09-978-522-3

```

```

Query Match 64.4%; Score 3011.5; DB 10; Length 859;
Best Local Similarity 64.9%; Pred. No. 3.5e-267;
Matches 547; Conservative 128; Mismatches 163; Indels 5; Gaps 3;

```

```

QY 41 KIKGKVIIMRSNVLPTEEHNSLNDNFTELLGGVSYFOLISATH--TSNDSRGKVGKAY 98
DB 17 KIKGTIVLMKKNVLPDNFNASVLRVHELLGGVPLQLVSAVHGDPANGLGKIGKAY 76
QY 99 LERWLTSIPLPAGESVFOINFQWDENFQFAGFIKNGHTSEFFLKSITLDDVPGYGRV 158
DB 77 LEDMITITSLTAGESAFKVTDFDDEIGECPAFIIRNNHHSEFYLRTLTLEDVPGRI 136
QY 159 HFDNCNSWVYPSGRYKDKRIFFAHVLPSQTPNPLRKYREELNWLSDGTGERKEWDRI 218
DB 137 HFVCSNWVYPAQHYKTDVFFTNQTYLPSETPGPLRKYREGELVNLRGDGTGELKEDRV 196
QY 219 YQYDVYNDIADP--DVGDHRPILGGTTEYPYPRGRGTRPRSRDRHNEYSRLSPIMSDI 276
DB 197 YQYAYNDLGNPDRLKYARVPLGSAEYYPYPRGRGTRGTPPEKDPNTESLPLAWSNI 256
QY 277 YPKDENFGLKMSDFLGYTLKALSISIKPGLQSIQFVTENEFDNFKEVDNLPERGPIPF 336
DB 257 YVPRDERFGLKMSDFLAYALKSIVQFLPEPEALCDITHNEFDFQDVLDIYEGGIKVP 316
QY 337 FNAFKTLTDLTP-PLFKALVNDGGEKFLKPTPEVWKNKIGWSTDBEFAREMLAGNPN 395
DB 317 EGPLLDKIKONTIPLMKELVTDGHELFKPNPQVIKEDKSAWTDDEFAEMLAGNPN 376
QY 396 LIIRLEAPPTSKLDPNVYGNQNSTITEEHKGLDGLTVDEAMKQNRXYIVDPHDALM 455
DB 377 VVIRLQEPFKSKLDPEVYGNQNSITKEHTENHLLDITINEAMEKRLFLDHDHDFM 436
QY 456 PYLTRNATSTKYATRTLLKDDGTLPVIELALPHQDQOLGALSILYFPAENGVO 515
DB 437 PYLRINTTSTKYASRTLLFLKDDGTLPKPLALELSLPHPSGDKFCANVKVTPAENGVE 496
QY 516 KSIWOLAKAYVTVNDVGHQLISHLHTHAVLEPVIATHRQLSVLHPHKLIVPHYKDT 575
DB 497 GSIWOLAKAYAAVNDVGHQLLSHNLNTHAATEPVIATNRQLSVLHPHKLIVPHYKDT 556
QY 576 MFINASARQVLINANGLIETHYPSKYSMELSSILYKDWTPDOALPNNLMKRGGLAVEDS 635
DB 557 MNINALARQLINAGVWESVTFPSKYAMSSVYKDWLVTEQALPADLIKRGMAVEDS 616
QY 636 SAPHGLRLINDYPPAVDGLDIWSAIIKTWVQYCCLYKDDNAVQNDPELQSWNNELREK 695
DB 617 EAPHGLRLINDYPPAVDGLDIWSAIIKTWVQYCCLYKDDNAVQNDPELQSWNNELREK 676
QY 696 GHADKXHPWPMQOTSELIESCTTIITIASALHAANFGQYPCYGYILNRPPTSRPFME 755
DB 677 GHGDKDEPWPMPMTVKELIETCTIITIASALHAANFGQYPCYGYILNRPPTSRPFME 736
QY 756 PEVGTAEYKELESNPEKAFURTI CSEALQVLSIIEILSKHASDEVYLGORASIDWTS 815
DB 737 PEEGTPEYELKSNPDKAFKLTITATQLLIGISLIEVLRSHSSEVYLGQDTEWTL 796
QY 816 KIALEAFKFKGNLFVEVENRIME RNKEVNLKNSGPNVLPYTLVPSSNEGTLGRGIPNS 875
DB 797 TTPKAFKFKGRKLADIEMMIIDRNNGNERFKNRVGPVKIPYTLVPSSNEGTLGRGIPNS 856
QY 876 ISI 878
DB 857 VSI 859

```

## RESULT 3

US-09-978-522-1



Db 506 GQYGAISKVYTPVBOG:ENSWOLAKAYVVDVSGYHQLISHWLTHAVIEPIILATNR 565  
QY 557 QLSVLHPHKLIVPHYKDTMTFNASARQVLINANGLIETTHYPKYSNELSSILYKDWTF 616  
Db 566 HUSVLHPHKLIVPHYKDTMTFNAGROILLNAGALELTVCPKYSNEFSVLYKDWVF 625  
QY 617 PDQALPNMLKRGKLAVEDSSAPHGLLELLINDYPFAVDGLDIWSAIKTWODYCCLYKDD 676  
Db 626 PEQALPEDLVKRGVAVKDSSTPYGLRLIEDYPFAVDGLEIWPALKTWKVDYCSFYKED 685  
QY 677 NAVQNDPELOSWNELREKGHADKHEPWPWPMQTLSELIESCTTIWIASALHAANFG 736  
Db 686 DTIKKDTBLQSWKKEIRVGHGDKDEPWPWPMQTLSELICTTCTTIWIASALHAANFG 745  
QY 737 QYPYGGYILNRRPTTSRRPWPVGTAEYKELESNPEKAPLRTICSELOALVSIIEILSK 796  
Db 746 QYPYGGFPSPRPAISRPPWPEKGTPEYDELVANPKAYLKVTSQFLAVLGISLVEILSK 805  
QY 797 HASDEVYLGQASIDWTSKIALEAFKFGKNLFEVENRINERKNVNLKNSGPNLPY 856  
Db 806 HSSDEVYLGQRTPDWTSABPLOAFKFGKGLADIBERILMNSDEKFRNRYGPNVMPY 865  
QY 857 TLLVPSSNEGLTGRGIPNSISI 878  
Db 866 TLLYPSKGGILTMGVFNSISI 887

RESULT 5  
US-10-424-599-215976  
; Sequence 215976, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424.599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 215976  
; LENGTH: 857  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_37056C.1.pap  
US-10-424-599-215976

Query Match 59.8%; Score 2795; DB 12; Length 857;  
Best Local Similarity 60.4%; Pred. No. 2.9e-247;  
Matches 525; Conservative 131; Mismatches 181; Indels 32; Gaps 7;

QY 28 GNILRVSSLOGNKIKGVILMRNSVLDFTBFHS-----NLLDNFTLGGG 74  
Db 3 GCLLHR-----GHKIKGTWLMRKNVLDVNSVTSVGGIIGQGLDVGSTLDTLTAFLGRS 57  
QY 75 VSPQLISATHNSDRSGVGNKAVLERWLTSIPPLFAGESVFOINFOWDENFGPPGAFPI 134  
Db 58 VSLQGISATKADANGKGLKATLEGITISLPTLGAGQSAFKINFWDGSGIPGAFYI 117  
QY 135 KNIGHTSEFFLKSLLDDVPYGRVHFCNSWVYPSGRYKDKRIFPANHVLPSQTNPLR 194  
Db 118 KNFMQTEFFLVSLTLEDIPNEGSIHFVNCNMIYNAKLFKSDRIFFANQTVLPSETPAVLV 177  
QY 195 KYREELNKLKRGDGTGERKEDRYDYVDYNDIADPDVGDH--RPILGCTTEYPYRGR 252  
Db 178 KYREELNKLKRGDGTGERKEDRYDYVDYNDLGDGPKNGENHARPVLGNDTPPYRGR 237  
QY 253 TGRPRSRDRHVESRLSPMSLDIYVPKDNFNGHKLKMSDFLGYTLKALSISIKPGLQSI 312

Db 238 TGRKPTRKDPNSES-----SNDVYLPRDEAFGHLKSSDFLTLYGLKSVSQNVLPQLQSAF 292  
QY 313 DV--TPNEBDFNPFVDNLPERGFPIPFNAFKTLTLEDLP-PLFKALVNDGCEKFLKPTTP 369  
Db 293 DLNFTPREDSFDEVHGLYGGIKLPTD-----IISKISPLVLKEIFFTDGEQALKFPP 348  
QY 370 EYVKNKIGWSTDEBFAREMLAGPNPLIRLEAPFPPTSKLDPNVYGNQNTTIEEHK 429  
Db 349 KVIQVSKSAMWTEBFAREMLAGVNPILRCLKDPFPRSKLDSQVYGDHSTQITKEHLEP 408  
QY 430 GUDGLTVDAMKONELYIVDPHDALMPYLTRNATSTKYATRTLLLLKDKDTLKPALIE 489  
Db 409 NLEGLTVDATONKRLFLDHDHDPIMPYLRRINATSTKAYATRTLLFKNDGTLPLALE 468  
QY 490 LALPHQDQDLGALISKLFPFAENGQKSIQWOLAKAYVTVNDVYHQLISHWLTHAVLEP 549  
Db 469 LSLPHQDQSGAFSQVFLPADGEGVSSIWLLAKAYVVVNDSCYHQLVSHMLNTHAVLEP 528  
QY 550 FVIATHRQLSVLHPHKLIVPHYKDTMTFNASARQVLINANGLIETTHYPKYSNELSSI 609  
Db 529 FIATNRHLSVVPHTYKLLHPHYRTMNINGLARLSLVNDGVIETQTLWGRYSVMSAV 588  
QY 610 LYKQMTFPDQALPNMLKRGKLAVEDSSAPHGLRLINDYPFAVDGLDIWSAIAIKTWQDYC 669  
Db 589 VYKDWVFTDQALPADLKEGMAIEDPSCPHGLRLVIEDYPYAVDGLEIWDALKTWVHEV 648  
QY 670 CLYKDDNAVQNDPELOSWNELREKGHADKHEPWPWPMQTLSELIESCTTIWIASAL 729  
Db 649 FLYKSDDTLREDPELOACWELVEVGHGDKNEPWPWPMQTLSELVEACAIITWASAL 708  
QY 730 HAAVNFQYYPGYILNRRPTTSRRPWPVGTAEYKELESNPEKAPLRTICSELOALVSI 789  
Db 709 HAAVNFQYYPGYILNRRPTTSRRPWPVGTAEYKELESNPEKAPLRTICSELOALVSI 768  
QY 790 IIEILSKHSDDEVYLGQASIDWTSKIALEAFKFGKNLFEVENRINERKNVNLKNS 849  
Db 769 VIEILSRHASDEVYLGQASIDWTSKIALEAFKFGKNLFEVENRINERKNVNLKNS 828  
QY 850 GPVNPYTLVLPSSNEGLTGRGIPNSISI 878  
Db 829 GPVNPYTLVLPSSNEGLTGRGIPNSISI 857

RESULT 6  
US-10-425-114-45769  
; Sequence 45769, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425.114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 45769  
; LENGTH: 860  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700675903\_FLI.pap  
US-10-425-114-45769

Query Match 59.8%; Score 2795; DB 12; Length 860;  
Best Local Similarity 60.4%; Pred. No. 2.9e-247;  
Matches 525; Conservative 131; Mismatches 181; Indels 32; Gaps 7;

QY 28 GNILRVSSLOGNKIKGVILMRNSVLDFTBFHS-----NLLDNFTLGGG 74

```
Db 6 GGLLHR-----GHKIKGTIVLMKKNVLDVNSVTVSGGIIGQGLDLVGSTLTDTLTAFLGRS 60
QY 75 VSFQIISATHTSNDSRGKVGKAYLERWLTSIPPLFAGESVFOINQFOWDENPFGPGAFFI 134
Db 61 VSLQIISATKADANGKGLKATFLEGIITSPLTLGAGQSAFKINFEDWDGSGIPGAFYI 120
QY 135 KNIGHTSERFLKSLTDDVPGYGRVHFDNCNSWYPSGRYKORIFPANHVLPSOTNPRLR 194
Db 121 KNFMQTEFFLVSLTLEDIPNHGSIHFVCSNIYNAKLFSADRIFFANQTYLPSETAPLV 180
QY 195 KYREELWNLGSDGTGERKEWDRIDYDVNDIADPDVGDH--RPILGGTTEYPYPRGR 252
Db 181 KYREELNLNGSDGTGERKEWRIYDVYNDLGDPKGENHARPLVGGNDTTFYPRGR 240
QY 253 TGRPSRRDHNYESRLSPLMSLDIYVPKDNFGLHKMSDFLGYTLKALSISIKPGLOSIF 312
Db 241 TGRKPTRKDPNSESR-----SNDVYLPRDEAFGLKSSDFLTGLKSVSNVLPQLQSAF 295
QY 313 DV--TPNEFDNFKEVDNLFERGFPIPFNAFKTLTLEDLTP-PLFKALVRNDGKFKLPPTP 369
Db 296 DLNFTPREDFSDEVHGLYSGGIKLPTD-----IISKISPLPVKBEI FRTDGEQALKFPPP 351
QY 370 EWDKDKNGTDEEFAREMLAGNPLLIIRLEAFPTTSKLDPNVYQNSNTITEHKKH 429
Db 352 KVIQVKSAMWTDDEFAREMLAGVNPNIIRCLKDFPRSKLDSQVYGDHTSQITKEHLEP 411
QY 430 GLDGLTVDEAMKQNLIVDFHDALMPYLTRNATSTKYATRTLLLLKDDGTLKPLVIE 489
Db 412 NLEGLTVDEAIQNKLFLLDHDHPMPYLRIINATSTKAYATRTILFLKNDGTLRPLAIE 471
QY 490 LALPHQDQDLGALSKLYFPAENGVOKSIWOLAKAYVTVDVGYHQLISHMLHTHAVLEP 549
Db 472 LSLPHQDQSGAFSQVFLPADEGVESIWLLAKAYVVNDSCVHQVLSVHMLTHAVLEP 531
QY 550 FVIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLIINANGLIETHTHPSKYSMELSSI 609
Db 532 FIATNRHLSVVRPIYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTLFGLWGRYSVMSAV 591
QY 610 LYKDWTFDQALPNNLMKRGVAVDSAPHLRLILLINDYPAVDGLDIWKAITWVQDYC 669
Db 592 VYKDWVTFDQALPADLIRKGMIAEDPSCPHGIRLVIEDYPAVDGLDIWKAITWVHEVY 651
QY 670 CLYKXDDNAVQNDPELOQSWWNLREKGHADKKHEPWPMPKQTLSELIESCTTIITIASAL 729
Db 652 FLXYKSDDTLREDPELOQACWKELVGVGHGDKKNPEWPKMQTRLEELVEACAIITWASAL 711
QY 730 HAAVNFQGYPYGGYILNRPPTTSRRFMPVEVGTAEYKELESNPEKAFLETICSELOALVSI 789
Db 712 HAAVNFQGYPYGGYILNRPPTLSRRFMPPEKGSAYEELRKNPKQKAYLKTITPKFQTLIDL 771
QY 790 IIEILSKHASDEVYLGORASIDWTSKJALEAFKFGKNI FVEVNRIMERNKEVNLKRS 849
Db 772 VIEILSRHASDEVYLGERNPNWTSITALEAFKFGKNI FVEVNRIMERNKEVNLKRS 831
QY 850 GPVNLPTYLLVPSSNEGLTGRGIPNSISI 878
Db 832 GPVQMPYTLPLPSKKEGLTFRGIPNSISI 860
```

## RESULT 7

```
US-10-425-114-54429
; Sequence 54429, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
```

```
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54429
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700842448_FLI.pap
US-10-425-114-54429
```

Query Match 59.8%; Score 2795; DB 12; Length 863;

Best Local Similarity 60.4%; Pred. No. 2.9e-241;

Matches 525; Conservative 131; Mismatches 181; Indels 32; Gaps 7;

```
QY 28 GNILDRVSLGNGKIKGVILMRSNVLDPTBFHS-----NLLDNFTLLGGG 74
Db 9 GGLLHR-----GHKIKGTIVLMKKNVLDVNSVTVSGGIIGQGLDLVGSTLTDTLTAFLGRS 63
QY 75 VSFQIISATHTSNDSRGKVGKAYLERWLTSIPPLFAGESVFOINQFOWDENPFGPGAFFI 134
Db 64 VSLQIISATKADANGKGLKATFLEGIITSPLTLGAGQSAFKINFEDWDGSGIPGAFYI 123
QY 135 KNIGHTSERFLKSLTDDVPGYGRVHFDNCNSWYPSGRYKORIFPANHVLPSOTNPRLR 194
Db 124 KNFMQTEFFLVSLTLEDIPNHGSIHFVCSNIYNAKLFSADRIFFANQTYLPSETAPLV 183
QY 195 KYREELWNLGSDGTGERKEWDRIDYDVNDIADPDVGDH--RPILGGTTEYPYPRGR 252
Db 184 KYREELNLNGSDGTGERKEWRIYDVYNDLGDPKGENHARPLVGGNDTTFYPRGR 243
QY 253 TGRPSRRDHNYESRLSPLMSLDIYVPKDNFGLHKMSDFLGYTLKALSISIKPGLOSIF 312
Db 244 TGRKPTRKDPNSESR-----SNDVYLPRDEAFGLKSSDFLTGLKSVSNVLPQLQSAF 298
QY 313 DV--TPNEFDNFKEVDNLFERGFPIPFNAFKTLTLEDLTP-PLFKALVRNDGKFKLPPTP 369
Db 299 DLNFTPREDFSDEVHGLYSGGIKLPTD-----IISKISPLPVKBEI FRTDGEQALKFPPP 354
QY 370 EWDKDKNGTDEEFAREMLAGNPLLIIRLEAFPTTSKLDPNVYQNSNTITEHKKH 429
Db 355 KVIQVKSAMWTDDEFAREMLAGVNPNIIRCLKDFPRSKLDSQVYGDHTSQITKEHLEP 414
QY 430 GLDGLTVDEAMKQNLIVDFHDALMPYLTRNATSTKYATRTLLLLKDDGTLKPLVIE 489
Db 415 NLEGLTVDEAIQNKLFLLDHDHPMPYLRIINATSTKAYATRTILFLKNDGTLRPLAIE 474
QY 490 LALPHQDQDLGALSKLYFPAENGVOKSIWOLAKAYVTVDVGYHQLISHMLHTHAVLEP 549
Db 475 LSLPHQDQSGAFSQVFLPADEGVESIWLLAKAYVVNDSCVHQVLSVHMLTHAVLEP 534
QY 550 FVIATHRQLSVLHPHKLIVPHYKDTMFINASARQVLIINANGLIETHTHPSKYSMELSSI 609
Db 535 FIATNRHLSVVRPIYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTLFGLWGRYSVMSAV 594
QY 610 LYKDWTFDQALPNNLMKRGVAVDSAPHLRLILLINDYPAVDGLDIWKAITWVQDYC 669
Db 595 VYKDWVTFDQALPADLIRKGMIAEDPSCPHGIRLVIEDYPAVDGLDIWKAITWVHEVY 654
QY 670 CLYKXDDNAVQNDPELOQSWWNLREKGHADKKHEPWPMPKQTLSELIESCTTIITIASAL 729
Db 655 FLXYKSDDTLREDPELOQACWKELVGVGHGDKKNPEWPKMQTRLEELVEACAIITWASAL 714
QY 730 HAAVNFQGYPYGGYILNRPPTTSRRFMPVEVGTAEYKELESNPEKAFLETICSELOALVSI 789
Db 715 HAAVNFQGYPYGGYILNRPPTLSRRFMPPEKGSAYEELRKNPKQKAYLKTITPKFQTLIDL 774
QY 790 IIEILSKHASDEVYLGORASIDWTSKJALEAFKFGKNI FVEVNRIMERNKEVNLKRS 849
Db 775 VIEILSRHASDEVYLGERNPNWTSITALEAFKFGKNI FVEVNRIMERNKEVNLKRS 834
QY 850 GPVNLPTYLLVPSSNEGLTGRGIPNSISI 878
```





Db 349 KVIQVSKSAWMTDEPAREMLAGVNPNIIRCLKDPFPRSKLDQVGDHTSQIKHELEP 408  
Qy 430 GLDGLTVDEAMQNRLLVIVPHDMLPILTRMNATSTKATYATRLLLKDDGTLKPLVIE 489  
Db 409 NLEGLTVDEATONRLLFLDHDHPIMPYLRINATSTKAYATRTILFLKNDGTLPLAIE 468  
Qy 490 LALPHQDQDOLGATSKLYFPAENGVOKSIWOLAKAYTVNDVGVHQLISHWLHATHVLEP 549  
Db 469 LSLPHQDQDQSGAFSFLPADEGVSSIWOLAKAYTVNDVGVHQLISHWLHATHVLEP 528  
Qy 550 FVIATHRQLSVLPHILKLLVPHYDXTMFINASAROVLINANGLIETTHYPSKYSMELSSI 609  
Db 529 FIATNRHLSVVPYIYKLLHPHYDXTMFINASAROVLINANGLIETTHYPSKYSMELSSI 588  
Qy 610 LYKDWTPDQALPNNLMKRGVAVDSAPHCRLRLINDYFPAVDGLDIWISAKITWVDYC 669  
Db 589 VYKDWVFDQALPADLIRKGMALIEDPSCPHGIRLVIEDYFPAVDGLDIWISAKITWVDYC 648  
Qy 670 CLYKDDNAVONDFELQSWNNELREKHAADKHPMPKMTLSLIESCTTIWIASAL 729  
Db 649 FLYYKSDTLREDPELQACWKELVEVGHGDKKNEPMPKMTLSLIESCTTIWIASAL 708  
Qy 730 HAAVNFQGYPGVILNRPTRSPMPVEVGTAEYKELESNPEKAFATICTSELOALVSI 789  
Db 709 HAAVNFQGYPGVILNRPTRSPMPVEVGTAEYKELESNPEKAFATICTSELOALVSI 768  
Qy 790 IIEILSKHASDEVYLGORASIDWTSKIALEAFKFKNLFVENRIMERKEVNLKRS 849  
Db 769 VIELSRHASDEVYGERNDPNWTSKIALEAFKFKNLFVENRIMERKEVNLKRS 828  
Qy 850 GPVNLPTVLLVPSNEGLTGRGIPNSISI 878  
Db 829 GPVQMPYVTLPLSPSKEGTLTFRGIPNSISI 857

## RESULT 10

US-10-424-599-215973  
; Sequence 215973, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 215973  
; LENGTH: 826  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_37053C.1.pep  
US-10-424-599-215973

Query Match 58.7%; Score 2742.5; DB 12; Length 826;  
Best Local Similarity 60.2%; Pred. No. 1.8e-242;  
Matches 515; Conservative 135; Mismatches 169; Indels 37; Gaps 9;

Qy 28 GNILDRVSSLGKNIKGVILMRSNVLDFTFEHNLNDNTELLGGGVSQLISATHSN 87  
Db 3 GGLIHR-----GHKIKGVILMRKNVLD-----VNSVTSV--GGIIGQA----- 39  
Qy 88 DSRGKGVNKAYLERWLTSIPPLFAGESVQINFQWENFGPPGAFKNGHTEFFLKL 147  
Db 40 NGKGLKATLEGITSLPLTGAGQSAFKINFEDDGGIPGAFYKFNFMQTEFFVL 99  
Qy 148 TLDDVPVGVGRVHFCNSWVPSGKYKDRIPFAHNVLPQTPNPLRYEBELHNLRGD 207  
Db 100 TLEDIPNHGSHFVNCNSWIYNAKLFKDRIPFANQYLPSETPAPLVKYREBELHNL 159

Qy 208 GTGERKEWDRIVDYVYNDIADDPVGDH--APILGGTTEYYPYPRGRTGRPSRRDHNYE 265  
Db 160 GTGERKEWERYDYVYNDLGDGPKGENHARFVLGNDTFYPRGRTGRKPTRDPNSE 219  
Qy 266 SLSLSPIMSLDIYVPDENFGLKMSDFLGTYLTKALSISIKPGLOQSIQFV--TPNEFDNFK 323  
Db 220 SR-----SNDVYLPDEAFGLKSSDFLYTGLKSVSONVLPQLQSAFDLNTFPREFDSFD 274  
Qy 324 EVDNLFERGFPIPFNAFKLTLEDLP-PLFKALVRNDGEKFLKPTTPEVVKDKIKGWSTD 382  
Db 275 EYHGLYSGGIKLPD-----IISKISFLPVLEIFRTDGEQALKFPFPPKVIQVSKSAMMTD 330  
Qy 383 EFAREMLAGNPILIRLEAPPTSKLDPNVYGNQNSTITEEHKHLGDLGTVDEAMKQ 442  
Db 331 EFAREMLAGVNPILIRCLKEFPFRSKLDSQVIGDHTSQIKHELPNLEGLTVDEALQN 390  
Qy 443 NRYLIVDFHDALMPYLTRMNATSTKYATRTLLKDDGTLKPLVIELALPHPQDQJGA 502  
Db 391 KRLFLDHDHPIMPYLRINATSTKAYATRTILFLKNDGTLRPLAIELSLPHPQDQSGA 450  
Qy 503 ISKLFPBAENGVOKSIWOLAKAYTVNDVGVHQLISHWLHATHVLEPFIATHRQLSVLH 562  
Db 451 FSQVFLPADEGVSESIWLLAKAYVVVNDSCYHQLVSHWLHATHVVEPFIATNRHLSVHH 510  
Qy 563 PIHKLLVPHYKDTMTFINASAROVLINANGLIETTHYPSKYSMELSSILYKDWTFPDQALP 622  
Db 511 PIYKLLHPHYRTMNINGLARLSLVNDGGVLEQTLWGRYSVENSAVYKDWVTFDQALP 570  
Qy 623 NNLMKRGVAVDSAPHCRLRLINDYFPAVDGLDIWISAKITWVDYCCLYKDDNAVOND 682  
Db 571 ADLIRKGMALIEDPSCPHGIRLVIEDYFPAVDGLEIWDALKTWVHEVYVLYKSDTLRED 630  
Qy 683 FELQSWNNELREKHAADKHPMPKMTLSLIESCTTIWIASALHAAVNFQGYPGV 742  
Db 631 PELQACWKELVEVGHGDKKNEPMPKMTLSLIESCTTIWIASALHAAVNFQGYPGV 690  
Qy 743 YILNRPTRSPMPVEVGTAEYKELESNPEKAFATICTSELOALVSIIEILSKHASDEV 802  
Db 691 LILNRPTRSPMPVEVGTAEYKELESNPEKAFATICTSELOALVSIIEILSKHASDEV 750  
Qy 803 YLGORASIDWTSKIALEAFKFKNLFVENRIMERKEVNLKRSQVNLPTVLLVPS 862  
Db 751 YLGERNDPNWTSKIALEAFKFKNLFVENRIMERKEVNLKRSQVNLPTVLLVPS 810  
Qy 863 SNEGLTGRGIPNSISI 878  
Db 811 SKEGLTFRGIPNSISI 826  
RESULT 11  
US-10-425-114-45631  
; Sequence 45631, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 45631  
; LENGTH: 832  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700733503\_FLI.pep

US-10-425-114-45631

Query Match 58.7%; Score 2742.5; DB 12; Length 832;  
Best Local Similarity 60.2%; Pred. No. 1.8e-242;  
Matches 515; Conservative 135; Mismatches 169; Indels 37; Gaps 9;

QY 28 GNILDRVSSLGNGKIKGKVIKMSNVLDPTFEHNSLNDNFTELLGGVSPQLISAHTSN 87  
DB 9 GCLLH-----GHKIKGVVLMKRVNLS-----VNSVTSV--CGIIOQA-----45  
QY 88 DSRGVGNKAYLERMLTIPPLPAGESVQINQFOWDENFGPGGAFFIKNGHTSEFFLKSL 147  
DB 46 NKGKGLKATFLEGIITSLPILGQSAFAKINFEWDDGSGIPGAFYIKNFMQIEFFLVSL 105  
QY 148 TLDDVPGVGRVHFDGNSWVPSGRYKDRIFPANHVLPSQTPNPLRKRYEELWNLRGD 207  
DB 106 TLEDIPNHSIHFCVNSIYNKLFKSDRIFFANQTYLPSETPAPLVKYREEELHNLRGD 165  
QY 208 GTGERKEWDRIVDYVNDIADPDVGDH--RPILGGTTEYPPRRGRTGPRRRDHYE 265  
DB 166 GTGERKEWERYDYVNDLGDGPKGNHARPVLGGNDTFYPPRRGRTGPKTKDPNSE 225  
QY 266 SRLSPIMSLDIYVPKDNFGLKMSDFLGYTLKALSISIKPGLQSIQFV--TNEFDNFK 323  
DB 226 SR-----SNDVYLPRDEAFGLKSDSLTYGLKVSQNVLPQLQSAFNLNFTPREFDSFD 280  
QY 324 EVDNLFEESGPIPPNFAKTLTDLTP--PLFKALVRNDGEKFKLPTPEVVKDKNGIWSID 382  
DB 281 EVHGLYGGIKLPTD-----IISKISPGVPLKBIPTDGEQALKEPPPKVQVSKSAMTD 336  
QY 383 EEFAREMAGNPPLIRLEAPPTSKLDPNVYGNQNSTITEEHIKGLDGLTVDEAMKQ 442  
DB 337 EEFAREMAGVNPENLIRCLKEFPFPRSKLDSQVYGDHTSQITKEHLEPNLGLTVDEAIQN 396  
QY 443 NRIYIVDHDALMPYLFRMNAITKTATRTLLLLKDDGLTKPLVIELALPHQDGLGA 502  
DB 397 KRLFLDHDHDPIMPLRRINATSTKAVATRTILFLKNDGTLPLAIELSLPHQDQSGA 456  
QY 503 ISKLYFPAENGVSQSIWOLAKAYTVNDVGVHQLISHLHHAVALPEPFIATNRHLSVH 562  
DB 457 FSQVPLPADEGVESIIWLLAKAYVNDVSCYHQLVSHLWNTHAVVEPFIATNRHLSVH 516  
QY 563 PIHKLIVHYKDTMFINASARQVLIINANGLIETTHYPSKYSMELSSILYKDWTFDQALP 622  
DB 517 PIYKLLHPHYDRTWNINGLARLSLVNDGGVIEQTFLGRYSKVSMSAVVYKDWTFDQALP 576  
QY 623 NNLKRGGLAVSDSAPHGLRLILNDYPAVDGLDIWSAIKTWQDYCCLYKDDNAVOND 682  
DB 577 ADLIRKGNVAIEDPSCPHGIRLVIEDYPAVDGLDIWDAIKTWVHYVLYKSDDTLRED 636  
QY 683 FELOSWMNELREKGHADKKHPPWPKMOTLSELIESCTTIWIASALHAAVNFQPYGG 742  
DB 637 PELOACWKELVGVGDKNEPWPVKMOTREELVEACAIITWIASALHAAVNFQPYGG 696  
QY 743 YLNRPTTSRPFMEBVGTAEYKELSNPEKAFLETICSELOALVSIIEILSKHASDEV 802  
DB 697 LILNRPTLSRPFMEKGSAAEYELRKNPQKAYLTIITPKFTLIDLSVIELSRHASDEV 756  
QY 803 YLGORASIDWTSKIALEAFKFGKNIKFEVENRIMERNEKYNLKRSGPNLYTLVAPS 862  
DB 757 YLGERDNPWTSIDTRALEAFKFGKNGKLAQIENKLSERNDEKLRNRCGPVQMPYTLILPS 816  
QY 863 SNEGTLRGIPNSISI 878  
DB 817 SKBGTLFRGIPNSISI 832

RESULT 12

US-10-425-114-46828  
; Sequence 46828, Application US/10425114  
; Publication No. US20040034898A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 46828  
LENGTH: 864  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
; OTHER INFORMATION: Clone ID: 701040644\_FLI.pep  
US-10-425-114-46828

Query Match 58.0%; Score 2713.5; DB 12; Length 864;

Best Local Similarity 57.3%; Pred. No. 9.1e-240;  
Matches 497; Conservative 166; Mismatches 185; Indels 19; Gaps 11;

QY 23 VINAGGNILDRVSSLGNGKIKGKVIKMSNVLDPTFEHNSLNDNFTELLGGVSPQLISA 82  
DB 6 INEVANNQIVER-----SKRVKGRVVMKKGVLDFHDIKANVLDNRVHELLGKGVSLQLISA 60  
QY 83 THTSNDNRGKV--GNKAYLERMLTSTIPPLPA--GESVQINQFOWDENFGPGGAFFIKNGHTS 140  
DB 61 T--TPPAKGLRGKVANLERWVSTISLTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 119  
QY 141 EFLKSLTLDDVPGY--GRVHFDGNSWVPSGRYKDRIFPANHVLPSQTPNPLRKRYE 199  
DB 120 QVYLTLLIEDIPGHGDPVNFVCSWVYPAHYAHADVFFANKAYLPCHTPELAKPREQ 179  
QY 200 ELWNRGDOGTGERKWDRIYDYVNDIADPDVG--DH--RPILGGTTEYPPRRGRTGPR 257  
DB 180 ELKTLTCGFGKLNEDRVYDYAYTNDLGLPDDGPDYARPVLGG--SQPFYRRGRTSRPH 238  
QY 258 SRDRHNSRLSPIMSLDIYVPKDNFGLKMSDFLGYTLKALSISIKPGLQSIQFDTVPN 317  
DB 239 CKTDPKTESRLH--LNLNVYVPRDEQFCHVKFSDFLAYSLKSAQVLLPEIKSLCDKTIIN 297  
QY 318 EFDNPKVDNLFERGFPIPPNFAKTLTDLTP--PLFKALVRNDGEKFLKFTPEVVKDKN 376  
DB 298 EFDTEQDVLDIYEGSIKLPSPGLTSKLRKLVPEYELLRELIRNDGERFLKFPVPDVIKVS 357  
QY 377 IGWSTDESFAREMLAGNPPLIRLEAPPTSKLDPNVYGNQNSTITEEHIKGLDGLTV 436  
DB 358 TAWRTDESFAREMLAGVNPVIRRLQEPFPKSLDPSVIGDQTSIRATHIENSIDGLTI 417  
QY 437 DEAMQNRLYIVDHDALMPYLIRLEAPPTSKLDPNVYGNQNSTITEEHIKGLDGLTV 496  
DB 418 DEAIQNMELFILDHHDLMPIYSIRNSTNTKTATRTLLFLQDDGTLKFLAIELSLPHQ 477  
QY 497 GDOLCAISKLPFAENGVSQSIWOLAKAYTVNDVGVHQLISHLHHAVALPEPFIATNR 556  
DB 478 GEQHGAVSKVFTPAQEGSVASVWQAKAYAAVNDVSGVHQLVSHWLYTHAVLEPFIATNR 537  
QY 557 QLSVLHPIHKLIVHYKDTMFINASARQVLIINANGLIETTHYPSKYSMELSSILYKDWTF 616  
DB 538 QLSILHPIHKLKPHFRDTMHNALRHTLINAGVLEITVFPKGFALEMSVLYKSWVF 597  
QY 617 PDQALPNMLKRGKLAVEDSSAPHGIRLLINDYPAVDGLDIWSAIKTWQDYCCLYKDD 676  
DB 598 TEQALPADLLKRGVAIPDSSSRHGLRVIEDYPAVDGIEIWDIAETWVTEYCNFYTSN 657  
QY 677 NAVQNDPELQSWNELREKGHADKKHPPWPKMOTLSELIESCTTIWIASALHAAVNF 736  
DB 658 DMVEDSELQSWKKEVRNEGHGDLKDRNWWPDMKTKEELIHSCTIILWASAFHAAVNF 717  
QY 737 QVPYGGYILNRPTTSRPFMEBVGTAEYKELSNPEKAFLETICSELOALVSIIEILSK 796  
DB 717 QVPYGGYILNRPTTSRPFMEBVGTAEYKELSNPEKAFLETICSELOALVSIIEILSK 796

Db 718 QYPAGYLPNRPVTSRRFMEQPTPEYBELKSDPELAFKXITTAQFOTLVGVSLIEVLSR 777  
Qy 797 HASDEVYLGQASIDWTSKIALFAEFKFGKULFEVENRIMERNKEVNLKXRGSPVNLPI 856  
Db 778 HSTEYVLGQENPEWTLDAEPFAFERFRQKLEIEINIMERNKDKFRNRPVMPY 837  
Qy 857 TLLVPSNE---GLTGRGIPNSISI 878  
Db 838 TLLPNTSDYSREGGLTKGIPNSISI 864

RESULT 13  
US-10-424-599-220216  
; Sequence 220216, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 220216  
; LENGTH: 860  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(860)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_40885C.1.pep  
US-10-424-599-220216

Query Match 57.9%; Score 2706.5; DB 12; Length 860;  
Best Local Similarity 59.9%; Pred. No. 4e-239;  
Matches 513; Conservative 129; Mismatches 186; Indels 29; Gaps 7;

Qy 41 KIKKVLNRSNVLDFTEFFS-----NLLDNTELLGGVSVFQLSATHSN 87  
Db 14 KVGTIVLMKRVLDINSITSVRGLGTGINIGSTIDGLTSFLGRSVCLQLSATKADG 73  
Qy 88 DSRGKVGKAYLERWLSIPPLFAGESVFOINFOWDENFGPGAFFIKNGHTSEFFLKS 147  
Db 74 NGNGVVGKTYLEGIIISIPPLGAGQAFTHFENDADMGIPGAFLLIKVMQVELEVL 133  
Qy 148 TLDVPGVGRVHPCNSGWPSPGKRYKDRIPFANHVLPQOTNPLKRYEELNMLRGD 207  
Db 134 TLEDIPNQSMHFVCNSWVNSKYEKDRIFFASETVVPGETVPGPLVTVREAEALQALRG 193  
Qy 208 GTGRKEDWRIYDVNDIADPDVGDH--RPILGGTTEYEPYRGGTGRPRGRDHNYE 265  
Db 194 GTGRKEDWRIYDVNDIADPDVGDH--RPILGGTTEYEPYRGGTGRPRGRDHNYE 253  
Qy 266 SRLSPIMSLDITVYPKDNFGLKMSDFLGYTLKALSISIKPLGQSPDV--TPNEFDNF 323  
Db 254 K-----PGEAYIPDENFGLKSSDFLTYGLKSLTRSLPALKTVDINFTNEPDSFE 307  
Qy 324 EVDNLFERGFPIPNNAKTYLTEDITP-PLFKALVRNDGKELFAPTEPVVKDNKIGWSD 382  
Db 308 EVRALCEGIGKLPID----ILSKISIPFLVKELIFRTDGSVLFPSVPLDIKVKSGAWMTD 363  
Qy 383 BEFAREMLAGNPLILRLAEFPPTSKLDPNVYQNSSTIEBHKHGLDGLTVDEAMQ 442  
Db 364 BEFAREMIAGNVPVIRLQEPFQSKLDPSVYGDQSKMTIDHLEINLEGLTVDRKID 423  
Qy 443 NRLIVDFHDMPLVITMWN-ATSKTYATRTLLLLKDDGTLKPLVITELALPHQGDQLG 501  
Db 424 QRLFDLHDDTFMPLRIDEKSKSKAYATRTILFLKDDGTLKPLVITELALPHQGDQLG 483

Qy 502 AISKLYFAENGQVKSIMOLAKAYVTVNDVGHQLIISHMLTHAVLEBPFVIATHRQLSVL 561  
Db 484 AYSKVLFPANQVESTIWLAKAHVIVNDSCVHQLISHMLTHAVIEBPFVIATNENLSIL 543  
Qy 562 HPIHKLVPHYKDTWFINASARQVLINANGLIETTHYPSKSMELSSILYKDWTPPDQAL 621  
Db 544 HPIYKLLPFHYRDTWNINALARQSLINADGFIKTFLGCKYAVEISSSGYKNWFLDQAL 603  
Qy 622 PNNMKRGLAVEDSSAPHGLRLINDYPAVDGLDWSAIIKTWQDQCCLYYKDDNAYON 681  
Db 604 PADLIRKGWAIEDSSCPNGLRLVIEDYPYAVDGLDWSAIIKTWQDQCCLYYKDDNAYON 663  
Qy 682 DEELQSMNELREKGHADKHEPWPKNQTLSELTESCTTIWIASAHAAVNEGQYVYG 741  
Db 664 DHELQAWKEVVERKGGDLKDKPWPKNQTLSELTESCTTIWIASAHAAVNEGQYVYG 723  
Qy 742 GYILNRPTTSRRFMEPEVGTAEYKELESNPEKAFRLTICSELQALVSIISILSKHASDE 801  
Db 724 GFILNRPTLSRWIPEEGTPEYDEMTKNPKQAYLRTITPKQALVDLSVIELSRHASDE 783  
Qy 802 VYLQORASIDWTSKIALFAEFKFGKULFEVENRIMERNKEVNLKXRGSPVNLPIYLVP 861  
Db 784 VYLQORDNPMTSNPKAIEAFKFGKLAETIKISERNHDPNLRNRTGPAQLPYVLLP 843  
Qy 862 SSNEGLTGRGIPNSISI 878  
Db 844 TSSETGLTFRGIPNSISI 860

RESULT 14  
US-10-424-599-239573  
; Sequence 239573, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 239573  
; LENGTH: 866  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_5835C.1.pep  
US-10-424-599-239573

Query Match 57.8%; Score 2700.5; DB 12; Length 866;  
Best Local Similarity 58.4%; Pred. No. 1.4e-238;  
Matches 513; Conservative 127; Mismatches 195; Indels 43; Gaps 7;

Qy 23 VINAGNILDVRSSVSGNKKIKGVILMRSNVLDFTEFH-----SNLL 64  
Db 10 ILNRG-----GCHKIKGTIVLMKRVLDNSVADLTKGNVGGGLIGTGLNVVGSTL 59  
Qy 65 DNFTTELLGGVSVFQLSATHSNDSRGKVGKAYLERWLSIPPLFAGESVFOINFOWDE 124  
Db 60 DNLTAFGRSVLQILSATKPLANGKVGKDKDTFLEGIIVSLPTLGAESAFNIOFENDE 119  
Qy 125 NFGFFGAFPIKNGHTSEFFLKSILTDVPGYGRVHFDCNSWYPSGRYKDRIPFANHY 184  
Db 120 SMGIPGAFYIKVMQVEFLKSLTLEDVFNQGTIRFCVNSWYNTKLYKSVRIFPANTY 179  
Qy 185 LPSQTNPLKRYEELNMLRGDGTGERKEDWRIYDVNDIADPDVGDH--RPILGGT 242  
Db 180 VPESTPAALVGYREBELNLRGDKGERKEDWRIYDVNDIADPDVGDH--RPILGGT 239



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2004, 11:51:28 / Search time 40.0332 Seconds  
(without alignments)  
2109.655 Million cell updates/sec

Title: US-09-937-908-1  
Perfect score: 4675  
Sequence: 1 MFGIGKNIIEGALNTTGDLA.....LVPSSNEGLTGRGIPNSISI 878

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4675	100.0	878	2 S74207	lipoxigenase (EC 1
2	3657.5	78.2	877	2 T10085	lipoxigenase (EC 1
3	2948.5	63.1	862	2 T07775	lipoxigenase (EC 1
4	2932	62.7	861	2 S44940	lipoxigenase (EC 1
5	2911	62.3	862	2 S57964	lipoxigenase (EC 1
6	2847	60.9	859	1 JQ2267	lipoxigenase (EC 1
7	2813.5	60.2	859	2 T06352	lipoxigenase (EC 1
8	2812.5	60.2	859	2 T06339	lipoxigenase (EC 1
9	2776	59.4	857	2 S01864	lipoxigenase (EC 1
10	2705.5	57.9	864	1 S07075	lipoxigenase (EC 1
11	2705	57.9	876	2 T07101	lipoxigenase (EC 1
12	2696.5	57.7	861	1 S01142	lipoxigenase (EC 1
13	2690	57.5	865	1 DASV11	lipoxigenase (EC 1
14	2663	57.0	865	2 T11852	lipoxigenase (EC 1
15	2649	56.7	859	2 T06429	lipoxigenase (EC 1
16	2644.5	56.6	864	2 S13381	lipoxigenase (EC 1
17	2640.5	56.5	858	2 T12142	lipoxigenase (EC 1
18	2634.5	56.4	856	2 T06596	lipoxigenase (EC 1
19	2632.5	56.3	868	2 T06897	lipoxigenase (EC 1
20	2596	55.5	862	2 S22153	lipoxigenase (EC 1
21	2591	55.4	853	2 T07662	lipoxigenase (EC 1
22	2582.5	55.2	839	1 DASV02	lipoxigenase (EC 1
23	2577	55.1	853	2 T07036	lipoxigenase (EC 1
24	2571	55.0	839	2 T06354	lipoxigenase (EC 1
25	2567	54.9	866	2 T06454	probable lipoxigen
26	2494.5	53.4	868	2 S56655	lipoxigenase (EC 1
27	2438	52.1	862	2 T05941	lipoxigenase (EC 1
28	2424	51.9	864	2 T05945	lipoxigenase (EC 1
29	2415	51.7	741	2 S18906	lipoxigenase (EC 1

30	2390.5	51.1	865	1 S23454	lipoxigenase (EC 1
31	2378	50.9	876	2 T05943	probable lipoxigen
32	1929.5	41.3	599	2 S18612	lipoxigenase (EC 1
33	1869	40.0	914	2 T07065	probable lipoxigen
34	1843	39.4	908	2 T07409	lipoxigenase (EC 1
35	1822.5	39.0	926	2 E96749	probable lipoxigen
36	1759.5	37.6	899	2 T07062	probable lipoxigen
37	1740	37.2	896	2 JQ2391	lipoxigenase (EC 1
38	1740	37.2	899	2 T11578	probable lipoxigen
39	1737.5	37.2	896	2 T07408	lipoxigenase (EC 1
40	1674	35.8	917	2 B96699	probable lipoxigen
41	1652	35.3	923	2 A53054	lipoxigenase (EC 1
42	1629	34.8	870	2 T47454	lipoxigenase ATLOX
43	1568.5	33.6	517	2 T06274	probable lipoxigen
44	1562	33.4	623	2 T07664	lipoxigenase (EC 1
45	1532.5	32.8	936	2 T06190	lipoxigenase (EC 1

ALIGNMENTS

RESULT 1

S74207  
lipoxigenase (EC 1.13.11.12) - cucumber  
C;Species: Cucumis sativus (cucumber)  
C;Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 20-Jun-2000  
C;Accession: S74207; S74137  
R;Hoehne, M.; Nellen, A.; Schwennesen, K.; Kindl, H.  
Eur. J. Biochem. 241, 6-11, 1996  
A;Title: Lipid body lipoxigenase characterized by protein fragmentation, cDNA sequence  
A;Reference number: S74137; MUID:97054584; PMID:889881  
A;Accession: S74207  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-878 <HOE>  
A;Cross-references: EMBL:X92890; NID:G1296511; PIDN:CA63483.1  
A;Experimental source: tissue cotyledones; clone PCSLBLOX221  
A;Accession: S74137  
A;Molecule type: protein  
A;Residues: 196,'X',198-204;218,'FX',221-223,'XX',226-228;305-309,'XX',312-316;441-460;  
C;Superfamily: lipoxigenase  
C;Keywords: oxidoreductase

Query Match	100.0%;	Score 4675;	DB 2;	Length 878;
Best Local Similarity	100.0%;	Pred. No. 1e-310;		
Matches 878;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MFGIGKNIIEGALNTTGDLAGSVINAGNILDVSSLGSKIKGKVIILMRSNVLDFTBFH	60	
Db	1	MFGIGKNIIEGALNTTGDLAGSVINAGNILDVSSLGSKIKGKVIILMRSNVLDFTBFH	60	
QY	61	SNLLDNFTTELLGGVVSFOLISATHTSNDSRGKVGKAYLERWLTSIPPLFAGESVFOINF	120	
Db	61	SNLLDNFTTELLGGVVSFOLISATHTSNDSRGKVGKAYLERWLTSIPPLFAGESVFOINF	120	
QY	121	QWENFPGPGAFIKNGHTSEFFLKSITLDDVPGVGRVHFDNCNWSVPSGKDKRIFFA	180	
Db	121	QWENFPGPGAFIKNGHTSEFFLKSITLDDVPGVGRVHFDNCNWSVPSGKDKRIFFA	180	
QY	181	NHVILPSQTPNPLRYREELWNLEGGDTGERKEWDRIYDYVDVNDIADPPVGDHRPILG	240	
Db	181	NHVILPSQTPNPLRYREELWNLEGGDTGERKEWDRIYDYVDVNDIADPPVGDHRPILG	240	
QY	241	GTEPYPRRGRTGPRSRDRDHVSRSLPMSLDIYVPKDNFGLKMSDFGLVTKAL	300	
Db	241	GTEPYPRRGRTGPRSRDRDHVSRSLPMSLDIYVPKDNFGLKMSDFGLVTKAL	300	
QY	301	SISIKPGQSIPDVTNPFDFNFKVDNLFERGFPTPFNAFKTLTDLTPPLFKALVRNDG	360	
Db	301	SISIKPGQSIPDVTNPFDFNFKVDNLFERGFPTPFNAFKTLTDLTPPLFKALVRNDG	360	
QY	361	EXFLKPTPEVVYDKNKGWSTDEEPAREMLAGPPLLRLEAFPTSKLDPNVYGNQNS	420	

Db 361 EKFLKFTPEVVVYKONKIGWSTDEBFAREMLAGNPLLIIRLEAPPTSKLDPNVYGNQNS 420  
QY 421 TITEBHIKHGLDGLTVDEAMKONRLYIVDFHDLMPYLTRMNATSTKYATRTLLIKDD 480  
Db 421 TITEBHIKHGLDGLTVDEAMKONRLYIVDFHDLMPYLTRMNATSTKYATRTLLIKDD 480  
QY 481 GTLKLPLVIELALPHPOGQOLGAI SKLYPPAENGVOKSIWOLAKAYVTVNDVGHQLISHW 540  
Db 481 GTLKLPLVIELALPHPOGQOLGAI SKLYPPAENGVOKSIWOLAKAYVTVNDVGHQLISHW 540  
QY 541 LHTHAVLEPFIATHRQSLVLPKHLVPHYKDTMFINASAROVLINANGLIETHYPS 600  
Db 541 LHTHAVLEPFIATHRQSLVLPKHLVPHYKDTMFINASAROVLINANGLIETHYPS 600  
QY 601 KYSMELSSILYKDWTFPDQALPNNLMKRGGLAVEDSSAPHGLRLLLINDYPPAVDGLDIWSA 660  
Db 601 KYSMELSSILYKDWTFPDQALPNNLMKRGGLAVEDSSAPHGLRLLLINDYPPAVDGLDIWSA 660  
QY 661 IKTWQDYCCLYYKDDNAVQNDPELOSWWNELEKRGHADKKHBPWPKMOTLSLIESCT 720  
Db 661 IKTWQDYCCLYYKDDNAVQNDPELOSWWNELEKRGHADKKHBPWPKMOTLSLIESCT 720  
QY 721 TIITIASALHAANVFGQYPYGGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAPLRTICS 780  
Db 721 TIITIASALHAANVFGQYPYGGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAPLRTICS 780  
QY 781 ELQALVSIISIELSKHASDEVYLGORASIDWTSKIALEAFKPGKULFEVENRIMERN 840  
Db 781 ELQALVSIISIELSKHASDEVYLGORASIDWTSKIALEAFKPGKULFEVENRIMERN 840  
QY 841 KEVNLKNSGPNVLPYTLVPSNEGTLGRGIPNSISI 878  
Db 841 KEVNLKNSGPNVLPYTLVPSNEGTLGRGIPNSISI 878  
RESULT 2  
T10085  
lipoxigenase (EC 1.13.11.12) - cucumber  
C:Species: Cucumis sativus (cucumber)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: T10085  
R:Matsui, K.; Nishio, M.; Kajiwara, T.; Hase, T.  
submitted to the EMBL Data Library, September 1995  
A:Reference number: Z16939  
A:Accession: T10085  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-877 <MAT>  
A:Cross-references: EMBL:U36339; NID:g1017771; PID:g1017772  
A:Experimental source: cv. Suoyo; tissue type root  
C:Function:  
A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis per  
C:Superfamily: lipoxigenase  
C:Keywords: fatty acid oxidation; oxidoreductase  
Query Match 78.2%; Score 3657.5; DB 2; Length 877;  
Best Local Similarity 76.2%; Pred. No. 2.7e-241;  
Matches 671; Conservative 105; Mismatches 99; Indels 5; Gaps 4;  
QY 1 MFGIGKNIIEGALNTTGLAGSVINAGNLDVRSSLGKNIKGVILMRSNVLDFTTEFH 60  
Db 1 MFSIGNIIEGALNTTGLAGSVINAGNLDVRSSLGKNIKGVILMRSNVLDFTTEFH 60  
QY 61 SNLLDNFTLEGGVSVFOLISATHTSN-DSRGKVNKAYLERWLTSTIPPLFAGESVFOIN 119  
Db 61 SLLDNFTLEGGVSVFOLISATHTSN-DSRGKVNKAYLERWLTSTIPPLFAGESVFOIN 120  
QY 120 FOWDENFGPGGAFFIKNGHTSEFFLKSITLDDVPGYGRVHFDCNSWYPSGRYKDKRIFF 179  
Db 121 FTWEGFGPGGAFFIKNGHTSEFFLKSITLDDVPGYGRVHFDCNSWYPSGRYKDKRIFF 180  
QY 180 ANHVLPSTQPNPLKRYEELWNLRGDGTGERKEWDRIYDYVNDIADPDVGDHHPIL 239

Db 181 ANNVLPSTQPNPLKRYEELWNLRGDGTGERKEWDRIYDYVNDIADPDVGDHHPIL 238  
QY 240 GGTTEYPYPRGRTRGRPRSRDHNSRLSPIMSLDIYVVKDENFGHLKMSDFLGYTLKA 299  
Db 239 GG-SQFPYPRGRTRGRPRSRDHNSRLSPIMSLDIYVVKDENFGHLKMSDFLGYTLKA 297  
QY 300 LSISIKPGLOSTFDVTPNEFDNFKEVDNLFERGPIIPENAKTTLTDTLTPLEKALVRND 359  
Db 298 LVATVQPALVNVDFTPGFEFKFQVHNLVGGGVPLVDVFNRLTKDTTPMFFBELRTD 357  
QY 360 G-EKELKFTPTPEVVKDNKIGWSTDEBFAREMLAGNPLLIIRLEAPPTSKLDPNVYGNQ 418  
Db 358 NDQRLKSPQPVKEDKFAQOTDEBFAREMLAGNPLLIIRLEAPPTSKLDPNVYGNQ 417  
QY 419 NSTIITEHIEKHGLDGLTVDEAMKONRLYIVDFHDLMPYLTRMNATSTKYATRTLLIK 478  
Db 418 HSKITEEDIKSGLEGLTVAEALNQRLYLIDHDLMPYLTRMNATSTKYATRTLLIK 477  
QY 479 DDGTLKPLVIELALPHPOGQOLGAI SKLYPPAENGVOKSIWOLAKAYVTVNDVGHQLIS 538  
Db 478 NDGTLKPLVIELALPHPOGQOLGAI SKLYPPAENGVOKSIWOLAKAYVTVNDVGHQLIS 537  
QY 539 HMLHTHAVLEPFIATHRQSLVLPKHLVPHYKDTMFINASAROVLINANGLIETHY 598  
Db 538 HMLHTHAVLEPFIATHRQSLVLPKHLVPHYKDTMFINASAROVLINANGLIETHY 597  
QY 599 PSKYSMELSSILYKDWTFPDQALPNNLMKRGGLAVEDSSAPHGLRLLLINDYPPAVDGLDIW 658  
Db 598 QSKYAMELSSILYKDWTFPDQALPNNLMKRGGLAVEDSSAPHGLRLLLINDYPPAVDGLDIW 657  
QY 659 SAIKTWQDYCCLYYKDDNAVQNDPELOSWWNELEKRGHADKKHBPWPKMOTLSLIES 718  
Db 658 STIKTWVINYCSLYYKDDSAIQNDVDELQSWWKEVREKGVKDKONETWPKLQNFELVET 717  
QY 719 CTIIIIWIASALHAANVFGQYPYGGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAPLRTI 778  
Db 718 CTIIIIWIASALHAANVFGQYPYGGYILNRPPTTSRRFMPEVGTAEYKELESNPEKAPLRTI 777  
QY 779 CSELOALVSIISIELSKHASDEVYLGORASIDWTSKIALEAFKPGKULFEVENRIME 838  
Db 778 NSMLQTLGLVSLIELSRHASDEVYLGORASIDWTSKIALEAFKPGKULFEVENRIME 837  
QY 839 RNKEVNLKNSGPNVLPYTLVPSNEGTLGRGIPNSISI 878  
Db 838 RNKDVNLKNSGPNVLPYTLVPSNEGTLGRGIPNSISI 877  
RESULT 3  
T07775  
lipoxigenase (EC 1.13.11.12) LX-3 - potato  
C:Species: Solanum tuberosum (potato)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 08-Oct-1999  
C:Accession: T07775  
R:Kolomietz, M.V.; Hannapel, D.J.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z16124  
A:Accession: T07775  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-862 <KOL>  
A:Cross-references: EMBL:U60202; NID:g1407704; PIDN:AAB67865.1; PID:g1407705  
A:Experimental source: cv. Berolina  
C:Genetics:  
A:Gene: LX-3  
C:Function:  
A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis per  
C:Superfamily: lipoxigenase  
C:Keywords: fatty acid oxidation; oxidoreductase  
Query Match 63.1%; Score 2948.5; DB 2; Length 862;  
Best Local Similarity 63.2%; Pred. No. 6.3e-193;  
Matches 534; Conservative 138; Mismatches 166; Indels 5; Gaps 3;

QY 39 GNKIKGVILMRNVLDTEPHSNLNDFTTELLGGVSVFOLISATH--SNDSEKGVGNK 96  
Db 18 GKVKGTIVLMKKNVLDPNVNASLSDGVLEFLGKRVSLQISLVYHADPGNSLQGRSNP 77  
QY 97 AYLERWLTISIPPLFAGSVFQINFWNDENFGFPAGFIKNGHTSEFFELKSLITLDDVPGY 156  
Db 78 AYLEKWLITGSLVAGESAFDVTFDWDEDIGVPCAFIINNFHFNFFYKLSLTLEDVPHG 137  
QY 157 RVHFDCHSVWVPSGRYKDRIFFAHNVLPSTQTNPLRKRYBEELNWLNRGDGTGERKEWD 216  
Db 138 NVHFCVNSWVPAKKYSERIFFANQAYLPQETPEPLRNTREKELVNLGRNGKLBWEWD 197  
QY 217 RIYDYNVDIADPDVGDH--RPILGGTTEYPYPRGRGTGRPRSRDHHYESLSPTMSL 274  
Db 198 RVDYALYNDIGDEKQKQYARTILGGSAAEYPPRRGTGRKPKADPKSESRIPLMSL 257  
QY 275 DIYPKDNFGLKMSDFGLTKALSISIKPGLQSIQFVTPNEFDNFKEVDNLFERGFP 334  
Db 258 DIYVPRDERFHHKLSDFLTALKSIVQFLIPEFQALFDSPTDFDFEDFEDVLKLYEGGK 317  
QY 335 IFFNAF-KTLTDELTPPLFKALVNDGKFLKPTPEVVKDKIGWSTDEEFAREMLAGP 393  
Db 318 LPQGFFLKALDSDIPEILKEIITDGEKFKFTPOVQEDSGSWTDEEFAREMLAGV 377  
QY 394 NPLLRLEAPPTSKLDPNVYGNQSTITEEHIKHGLDGLTVDKAMQNRLYIVDPHDA 453  
Db 378 NPVIISRLQEPFQSDSEVYGNQSTITEEHIKGLDGLTDDAIKTNRLYILNHDI 437  
QY 454 LMPYLTRMNSTKYATRTLLLLKDDGTLKPLVIELALPHQDQGLGALSILYFPAENG 513  
Db 438 LMPYVRINTNTKLYASRTLLFLQDDGTWKPAIELSLPHQDDELGAWSKYVTPADQG 497  
QY 514 VQKSIWOLAKAYVTVNDVGVHOLISHWLHVALEPPVIATHRQLSVLHPIKLLVPHY 573  
Db 498 VEGSIWOLAKAYVAVNDVGVHQLISHWLHVALEPPVIATHRQLSVLHPIKLLHPPR 557  
QY 574 DTMFINASARVLNANGLIETHYPSKYSMELSSILYKDWTPPDQALPNMLMKRGGLAVE 633  
Db 558 DTMNALARQILINAGVLEMTVPKAYAMEMSAVYKSVVPEQALPADLIRGVAVE 617  
QY 634 DSSAPHLRLINDYPPAVDGLDLSWAIKTVWQDYCCLYKDDNAVQNDPELOSNNELR 693  
Db 618 DSSSPHGVRLLIQYPPAVDGLDLSWAIKSNVTEYCNFYKSDLVKDNELQAWKELR 677  
QY 694 EKHGADKXHEPWPWKMTLSLIESCTTIWIASALHAANVFGQYPYGGYILNRPTTSRR 753  
Db 678 EKHGADKDEPWPWKMTQRLKDSCTIIWIASALHAANVFGQYPYAGYLPNRPILSR 737  
QY 754 FMPVGTAEYKELSNPEKFLRTICSELQALVSIISIIELSKHASDEVYLGORASDWT 813  
Db 738 FMPSPGTPEYBELKTNPDKAYLKTITPOLQTLGSLIELSRHASDEIYLGORDSEWT 797  
QY 814 SDKIALFAFEKGNLFEVENRIMERNEKVNLRSGPVNLPTYLLVPSSNEGILTRGIP 873  
Db 798 KDQSPIAAFERFGKLSIEIQIIMQNGDKWKKNRSGPVNVVPTLLPPTSEQGLTGKIP 857  
QY 874 NSISI 878  
Db 858 NSVSI 862

## RESULT 4

S44940

lipoxigenase (EC 1.13.11.12) - potato

C:Species: Solanum tuberosum (potato)

C:Date: 06-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 11-Jun-1999

C:Accession: S44940

R:Casey, R.

submitted to the EMBL Data Library, May 1994

A:Reference number: S44940

A:Accession: S44940

A:Molecule type: mRNA

A:Residues: 1-861 &lt;CAS&gt;

A;Cross-references: EMBL:X79107; NID:G486618; PIDN:CAA55724.1; PID:G486619  
C;Superfamily: lipoxigenase  
C;Keywords: oxidoreductase

Query Match 62.7%; Score 2932; DB 2; Length 861;  
Best Local Similarity 63.8%; Pred. No. 8.4e-192;

Matches 543; Conservative 124; Mismatches 174; Indels 10; Gaps 5;

QY 38 GGN----KIKGVILMRNVLDTEPHSNLNDFTTELLGGVSVFOLISATH--TSNDRG 91  
Db 11 GGHDSKKVKGTVVMNKNVLDFTDLAGSLTGKIFDVLGQKVSFQLISSVQDPTNGLQG 70  
QY 92 KVGNYKAYLERWLTISIPPLFAG--ESVQFNQFOWDENFGFPAGFIKNGHTSEFFELKSLTLD 150  
Db 71 KSNPAYLENSLFTITPLTAGSETAFGVTFDWNEEFVGPAGFIKKNMINFEFFLKSILIE 130  
QY 151 DVPYGRVHFDCHSVWVPSGRYKDRIFFAHNVLPSTQTNPLRKRYBEELNWLNRGDGTG 210  
Db 131 DVNHEGVHFCVNSWVPAKKYSERIFFANQAYLPQETPEPLRNTREKELVNLGRNGKLBWDGTG 190  
QY 211 ERKEWDRIVYDYNVDIADPDVGDH--RPILGGTTEYPYPRGRGTGRPRSRDHHYESRL 268  
Db 191 KKEADWRIYDYNVDIADPDVGDH--RPILGGTTEYPYPRGRGTGRPRSRDHHYESRL 250  
QY 269 SPIMSLDIYVPKDNFGLKMSDFGLTKALSISIKPGLQSIQFVTPNEFDNFKEVDNL 328  
Db 251 PLISLSDIYVPRDERFHHKLSDFLTALKSIVQFLIPEFQALFDSPTDFDFEDFEDVLRL 310  
QY 329 FERGPPIPN--AFKILTDELTPPLFKALVNDGKFLKPTPEVVKDKIGWSTDEEFAR 387  
Db 311 YEGGKLPQGPFLKALTAAPLEMIRELLRTDGEILRFPTPLVTKDSKTAMRTDEEFAR 370  
QY 388 EMLAGNPLLRLEAPPTSKLDPNVYGNQSTITEEHIKHGLDGLTVDKAMQNRLYI 447  
Db 371 EMLAGNVPIISRLQEPFQSDSEVYGNQSTITEEHIKGLDGLTVDKAMQNRLYI 430  
QY 448 VFHDMPLTRMNSTKYATRTLLLLKDDGTLKPLVIELALPHQDQGLGALSILY 507  
Db 431 LNHHDVILPYLRIRINTITTKAYASRTLLFLQDNGSLKPLAIELSPHPDQGFVTSKVY 490  
QY 508 FPAENGVOKSINQALAKAYVTVNDVGVHOLISHWLHVALEPPVIATHRQLSVLHPIKL 567  
Db 491 TFSQGVESINQALAKAYVAVNDVGVHOLISHWLHVALEPPVIATHRQLSVLHPIKL 550  
QY 568 LVPHYKDTMFINASARQVLNANGLIETHYPSKYSMELSSILYKDWTPPDQALPNMLMK 627  
Db 551 LVPHFRDTMNINASARQLLVNAGGVLESTVFQSKFAMEMSAVYKDWVFPDQALPADLVK 610  
QY 628 RGLAYEDSSAPHLRLINDYPPAVDGLDLSWAIKTVWQDYCCLYKDDNAVQNDPELOS 687  
Db 611 RGVAVEDSSSPHGVRLLIQYPPAVDGLDLSWAIKSNVTEYCNFYKSDLVKDNELQAW 670  
QY 688 WNNELREKGHADKXHEPWPWKMTLSLIESCTTIWIASALHAANVFGQYPYGGYILNR 747  
Db 671 WNKELREVGHGDKKNEPWPMEETPQELIDSCCTTIWIASALHAANVFGQYPYAGYLPNR 730  
QY 748 PTTSRRFMPVGTAEYKELSNPEKFLRTICSELQALVSIISIIELSKHASDEVYLGOR 807  
Db 731 PTVSRFRFMPVGTAEYKELSNPEKFLRTICSELQALVSIISIIELSKHASDEVYLGOR 790  
QY 808 ASIDWTSKDIALEAFKGNLFEVENRIMERNEKVNLRSGPVNLPTYLLVPSSNEGIL 867  
Db 791 ESPEWTKDEPLAAFDKFKLTDIEKQIIQRNGDNILTRNSGPNVAPYLLPPTSEGL 850  
QY 868 TCRGIPNSISI 878  
Db 851 TCRGIPNSVSI 861

## RESULT 5

S57964

lipoxigenase (EC 1.13.11.12) - common tobacco

C:Species: Nicotiana tabacum (common tobacco)



C>Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 11-Jun-1999  
C/Accession: S57964  
R:Veronesi, C.; Fournier, J.; Rickauer, M.; Esquerre-Tugaye, M.T.  
submitted to the EMBL Data Library, January 1995  
A:Description: Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA.  
A/Reference number: S57964  
A/Accession: S57964  
A/Status: Preliminary  
A/Molecule type: mRNA  
A/Residues: 1-862 <VER>  
A/Cross-references: EMBL:X84040; NID:G899343; PIDN:CAA58859.1; PID:G899344  
C:Superfamily: lipoxigenase  
C:Keywords: oxidoreductase

Query Match 62.3%; Score 2911; DB 2; Length 862;  
Best Local Similarity 62.3%; Pred. No. 2.3e-190;  
Matches 534; Conservative 140; Mismatches 175; Indels 8; Gaps 6;

QY 30 ILDRVSSL-GGNKIKGKVKILMRSNVLDFTPEHNSNLDNFTTELLGGVSLFOLIGATHT--S 86  
DB 6 IVDALTGDDGKKVKGTVLMKNVLDFTDINASVGLGVLEFLGRRVSLSLISVNRADPA 65  
QY 87 NDSRGKGNKAYLERWLTISIPLFAGESVFOINFOW-DENPGFPGAFIKNGHTSEFLK 145  
DB 66 NGLOGKRSKAAAYLENWLTNSTPIAAGESAFRTVDWDEBFGVPGAFIINKLHFSBFLK 125  
QY 146 SLTLDVDPVGRVHFDNCNWSVYPSGRYKORIPFANHVLPSONPPLRKRYREELNLR 205  
DB 126 SLTLEDVNHGKRVHVCNWSVYPAKYKSDRIFFANQAYLPSETPDLRKIRENELVTLR 185  
QY 206 GDGTGERKEDRIYDYVDYNDIADPDVGD--HRPILGTTTEYPPYPRGRTGRPSRDHN 263  
DB 186 GDGTGKLEWRVYDYAYNDLGDPDKGQDLSRPVLAGSSEYPPYPRGRTGRKPTKDPN 245  
QY 264 YESRLSPMSLDIYVPKDNFCHLKMDSFLGYTLKALSISIKPGLQSIQFVTPNEFDNF 323  
DB 246 SESRIPLMSLDIYVPRDERFGHLKMSDFLTFAKLSIVQLLPBFAKLFDSSTNEFDSF 305  
QY 324 EVDNLFERGFPIFN-AFKTTEDLTPPLFKALVRNDGKFLKPTPEVVKDNKIGWSTD 382  
DB 306 DVLKLYEGGKLPQGPLLKAITDSIPLLEILKELRSDEGLFKYPTQVQLQEDKTAWRTD 365  
QY 383 BEFAREMLAGNPILIRLEAFPTSKLDPNVYGNQNSTITEEHIKGLDGLTVDEANMQ 442  
DB 366 BEFGREMLAGNPVILISLQEPFKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIRT 425  
QY 443 NRLYIVDFHDALMPYLTMN-ATSTKYATVATLRLLLKDDGLTKPLVLTELPHPQGDQLG 501  
DB 426 NRLFILNHHDLMPYLRLINTSTDTKYASRTLLFLQDNGTLKPSAIELSLPHPDGDQFG 485  
QY 502 AISKLYFAENGVOGKSIWQAKAVTVNDVGVYHOLISHWLTHAVLEPFIATHRLQSLVL 561  
DB 486 AVSKYVTPADQGVGSIWQAKAVAVNDGSIWQALSHWLTHAAIEPFIATNRQLSAL 545  
QY 562 HPIKHLVPHYKDMFNINASARQVLINANGLIETTHYPSKYSMBELSSILYKDMTFPDQAL 621  
DB 546 HPIYKLLHPHRETNNALARQLINGGGGLEUTVPFKYSMBGSAVYKDWVFFEQAL 605  
QY 622 FNNLMKRGVAVEDSSAPHLRLINDYPFAVDGLDIWSAINTWQDYCCLYKDDNAVQN 681  
DB 606 PTDILKRGVAVEDSSAPHLRLINDYPFAVDGLDIWSAINTWQDYCCLYKDDNAVQN 665  
QY 682 FDELQSWNEIREKHADKKEHPKMQTLSELIESCTTIIMTASALHAANVFGQYPYG 741  
DB 666 DTELQAWKEUREBGHGKDDPEPWPKNQTVQELIDICTITIMTASALHAANVFGQYPYA 725  
QY 742 GYLNRPTTSRRFPVGTABYKELESNPEKAFRLTICSELQALVSIISIEILSKIASDE 801  
DB 726 GYLNNRPTLSNFMFPERGSPYEELKTPDKVFLKTTTPQLQTLGLSIEILSRHSDT 785  
QY 802 VYLQASIDWTSKIALAEKFGKQLFVENRIMERNKEVNLKRSQVNPVLYLLVP 861  
DB 786 LYLQGRESPEWTKQEP-LSAFAREGKLSLIEDQIMQMVNDKWKNSRGPVKPYTLLFP 845

QY 862 SSNEGLTGKIPNSISIS 878  
DB 846 TSEGLTGKIPNSVSI 862

## RESULT 6

QJ02267  
lipoxigenase (EC 1.13.11.12) Lox1 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C/Accession: JQ2267  
R:Melan, M.A.; Dong, X.; Endara, M.E.; Davis, K.R.; Ausubel, F.M.; Peterman, T.K.  
Plant Physiol. 101, 441-450, 1993  
A:Title: An Arabidopsis thaliana lipoxigenase gene can be induced by pathogens, abscisic  
A/Reference number: JQ2267; MUID:94105302; PMID:7506426  
A/Accession: JQ2267  
A/Molecule type: mRNA  
A/Residues: 1-859 <MEL>  
A/Cross-references: GB:L04637; NID:G289202; PIDN:AAA32827.1; PID:G289203  
C/Comment: This enzyme catalyzes the hydroperoxidation of polyunsaturated fatty acids co  
C:Superfamily: lipoxigenase  
C:Keywords: fatty acid oxidation; oxidoreductase

Query Match 60.9%; Score 2847; DB 1; Length 859;  
Best Local Similarity 61.0%; Pred. No. 5.3e-186;  
Matches 525; Conservative 142; Mismatches 181; Indels 12; Gaps 7;

QY 28 GNILDRVSSLGN-----KIKGVLMRSNVLDFTPEHNSNLDNFTTELLGGVSLFOLISA 82  
DB 3 GELRDLLTG-GGNETTTTKKVGTVLMKNVLDNDFNASFLDLRHLHEFLGNKILRLVSS 61  
QY 83 --THTSNDSRGKVGKAYLERWLTISIPLFAGESVFOINFOWDENFGSPGAFIKNGHTS 140  
DB 62 DVTDSENGSKGLKAAHLEDWITITSLTAGESAFKVTFDYETDFGYPGAFIRNSHFS 121  
QY 141 EFLKSLTLDVDPVGRVHFDNCNWSVYPSGRYKORIPFANHVLPSONPPLRKRYREE 200  
DB 122 EFLKSLTLEDVPGHGRVHYICNSWIYPAKHYTTDRVFSNKTYLPHETATLLKYREE 181  
QY 201 LWNLRGDTGGERKEDRIYDYVDYNDIADPDVGRHPLGTTTEYPPYPRGRTGRPSRR 260  
DB 182 LVSLRGTEGELKEDRWYDYAYNDLGVPP-KNRPVVLGCTQYPPYPRGRTGRKPTKE 240  
QY 261 DHNYSRLSPIMSLDIYVPKDNFCHLKMDSFLGYTLKALSISIKPGLQSIQFVTPNEFD 320  
DB 241 DPQTESRLPITSSLDIYVPRDERFGHLKMDSFLAYALKAAIAQFIQPALEAVFDDTPKEFD 300  
QY 321 NFEKVDNLFERGFPIFNA-FKLTLEDLTPPLFKALVRNDGKFLKPTPEVVKDNKIGW 379  
DB 301 SPEDVLKIYEGIDILFNQALIDSIVKNIPLEMLKEIFRDCQKFLKFPVPIKEDKTAW 360  
QY 380 SPDEFAREMLAGNPILIRLEAFPTSKLDPNVYGNQNSTITEEHIKGLDGLTVDEA 439  
DB 361 RTDEFAREMLAGNPVILISLQEPFKSKLDSESYGNQNSTITKSHIEHNLGLTVEEA 420  
QY 440 MKQNLRYIVDFHDALMPYLTMNATSTKYATRLILLKDDGTGLKPLVIELALHPQGDQ 499  
DB 421 LEKERLFTLDHHDLTMPYLGRVNTTITKYASRTLLFLKDDGTGLKPLVIELSLHPHPGDK 480  
QY 500 LGAISKLYFAENGVOGKSIWQAKAVTVNDVGVYHOLISHWLTHAVLEPFIATHRLS 559  
DB 481 FGAVSEVTPGE-GYVDSLWQLAKAFVGVNDGSHQLISHWQTHASTEPFIATNRQLS 539  
QY 560 VLHPILKLLVPHYKDMFNINASARQVLINANGLIETTHYPSKYSMBELSSILYKDYD-WTFPD 618  
DB 540 VLHPVFKLLEPHFRDNNALARQLINGGGGLEUTVPFKYSMBGSAVYKDWVFFEQAL 599  
QY 619 QALPNLMKRGVAVEDSSAPHLRLINDYPFAVDGLDIWSAINTWQDYCCLYKDDNAVQ 678  
DB 600 QALPAELKRGVAVEDPEAPHLRLIKDYPYVDGLEVWVALESWVRDYLFLYKLEED 659  
QY 679 VQNDPELOSWNELREKHADKKEHPKMQTLSELIESCTTIIMTASALHAANVFGQY 738

Db 660 IQTTELOAWKVEVREHGDKKPEWPKQTEELVESCTIIWVASALHRAVNGQY 719  
QY 739 PYGGYILNRPRTTSRRFPEVGTATYKELESNPEKAFRTICSELOALVSIISIEILSKHA 798  
Db 720 PVAGYLPNRPRTISRQYXPKENTPFEFELEKKNPKDFVLKTTITAOQLTGLISLEILSTHS 779  
QY 799 SDEVYLGORASIDWTSKIALEAFKFGKLNLFVENRIMERNKEVNLKNSGPNVLPYTL 858  
Db 780 SDEVYLGORDSKWAEEKALAEKFGKVEKIEKIDERNDDTUKNTGLVYKMYTL 839  
QY 859 LVPSNEGLTGRGIPNSISI 878  
Db 840 LFPSEGGVTGRGIPNSVSI 859

RESULT 7  
T06352  
lipoxigenase (EC 1.13.11.12) - tomato  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000  
A;Accession: T06352  
R;Kausch, K.D.; Handa, A.K.  
Plant Physiol. 107, 669-670, 1995  
A;Title: Molecular cloning and nucleotide sequence of a lipoxigenase cDNA from ripening  
A;Reference number: Z15617; MUID:95241637; PMID:7724686  
A;Accession: T06352  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-859 <KAU>  
A;Cross-references: EMBL:U13681; NID:9534845; PIDN:AAA74939.1; PID:9534846  
A;Experimental source: strain Rutgers; tissue-type fruit pericarp  
C;Genetics: LOX  
A;Gene: LOX  
C;Superfamily: lipoxigenase  
C;Keywords: oxidoreductase

Query Match 60.2%; Score 2813.5; DB 2; Length 859;  
Best Local Similarity 60.9%; Pred. No. 1e-183;  
Matches 523; Conservative 140; Mismatches 185; Indels 11; Gaps 7;

QY 28 GNILDRVSSLGNN--KIKGVILMRNVLDFTFEHNLNDNFTELLGGVSGVQLISATH 84  
Db 4 GGIVDAI--LGKDRPKVKGVLMMKNVLDIFNIGASVVDGSDLLGQKVSQILISGV 61  
QY 85 TSNDRGKVGKNKAYLERWLTSIPPLFAGESVFQINFQWD--ENFGFPGAFFIKNGHTSEFF 143  
Db 62 NYDGLGKLSNPAYLESWLTDTITAGESTSVTFDWRDDEFQVGPVAFIKNLHNEFF 121  
QY 144 LKSLTLDVPGYGRVHFDGNSWVPSGRYKDKRIFFAHNVYLPSTQNPRLKRYREELWN 203  
Db 122 LKSLTLEDVPNYKIHFCVNSWVPAFRYKSDRIFFANQAYLPSETPQPLRKYRENELVA 181  
QY 204 LRGGDTGERKEWDRIYDVYNDIADPDVGDH--RPILGGTTEYPYPRRGTRGRPSRRD 261  
Db 182 LRGGDTGKLEWDVYACVNDLGECDKGEYARPIILGSSSEYFYPFRGRTGREPTKAD 241  
QY 262 HNYESRSLPMSLDIYVPKDNFGLKVDPLGLVTLKALISIKPGLQSFIDVTPNEFDN 321  
Db 242 PNCESRNPLMSLDIYVPRDRFRGHVKKSDPLTSSLSLQTLPLFAKALCDNTNEFNS 301  
QY 322 FKEVDNLPERGFPPENAF--KTLTDLTLPFLKALVNDGDKFLKFTPEVVKDNKIGWS 380  
Db 302 FADVLNLYEGGIKLPFGFWLKAIDNISSEILKDLQTDGGLGLKYTPPQIQDKTAWR 361  
QY 361 TDEFAREMLAGPNLLIRLEAPPTSKLDPNYGNQNSITTEHFKHGLDGLTVDEAM 440  
Db 362 TDEFGRMLAGSNPLVLSRLOEFPFKSKLDPTIYGNQNSITTEHVQDKLGLTVNEAI 421  
QY 441 KQNELYIVDFDALMPYLTRNN--ATSKTYATRLALLKODGTGLKPLVIELALPHPOGQ 499  
Db 422 KSNRLFILNHDIWNPLLRKINNSANTKAYASRTLLFLQDDRTLUKPLAIELSUPHPDQ 481

QY 500 LGAISLKYPAENGQVQKSIWQAKAYTVTVNDVGYHQLISHWLHTHAVLEPFIATHRQLS 559  
Db 482 FGTQSVKYVTPADQGVGSIWQFAKAYAVVNDMGHQLISHWLHTHAVLEPFIATHRQLS 541  
QY 560 VLHPHKLVLVPHYKDTMTFINASAROVNLNANGLIETTHYPSKYSMELSSILYKDWTFPDQ 619  
Db 542 VLHPHKLVLVPHFRNTMINALARETL--TYDGGFTSLFPAPKYSNEMGAAA-KDWVFEQ 600  
QY 620 ALPNMIMKGLAVESSAPHGRLRLINDYPPAVDGLDIWSAIKTWVQYCCLYKDDNAV 679  
Db 601 ALPADLLKRGVAVEDLSLSPHGIRLLILDYPAVDGLEIWAATKSWVTYCKFYKSDTV 660  
QY 680 QNDFELOSWNELREKHKHADKKHPEWPKMQTSLIESCTTIWIASALHAAVNFQVY 739  
Db 661 EKDTLOAWKELREHGCDKDEAWNPKLQTRQELRDCCTIIWIASALHAALEFGLYS 720  
QY 740 YGGYILNRPRTTSRRFPEVGTATYKELESNPEKAFRTICSELOALVSIISIEILSKHAS 799  
Db 721 YAGYLPNRPRTLSNLMPPSPGSVEYBELKTNPKVFLKTFVPLQSLLSISIFEVSSRUAS 780  
QY 800 DEVYLGORASIDWTSKIALEAFKFGKLNLFVENRIMERNKEVNLKNSGPNVLPYTL 859  
Db 781 DEVYLGORDSIEWTKDEPLVAFERFGKMLSDIENRIMMNSHKSKWKNRSGPNVLPYTL 840  
QY 860 VFSSNEGLTGRGIPNSISI 878  
Db 841 FPTSSEGLTGKIPNSVSI 859

RESULT 8  
T06339  
lipoxigenase (EC 1.13.11.12) loxB - tomato  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000  
C;Accession: T06339  
R;Ferrie, B.J.; Beaudoin, N.; Burkhardt, W.; Bowsher, C.G.; Rochstein, S.J.  
Plant Physiol. 106, 109-118, 1994  
A;Title: The cloning of two tomato lipoxigenase genes and their differential expression  
A;Reference number: Z15612; MUID:95062736; PMID:7972514  
A;Accession: T06339  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-859 <PER>  
A;Cross-references: EMBL:U09025; NID:9575431; PIDN:AAA3103.1; PID:9482901  
A;Experimental source: strain Caruso; tissue-type fruit pericarp  
C;Genetics: loxB  
A;Gene: loxB  
C;Superfamily: lipoxigenase  
C;Keywords: oxidoreductase

Query Match 60.2%; Score 2812.5; DB 2; Length 859;  
Best Local Similarity 60.8%; Pred. No. 1.2e-183;  
Matches 522; Conservative 141; Mismatches 185; Indels 11; Gaps 7;

QY 28 GNILDRVSSLGNN--KIKGVILMRNVLDFTFEHNLNDNFTELLGGVSGVQLISATH 84  
Db 4 GGIVDAI--LGKDRPKVKGVLMMKNVLDIFNIGASVVDGSDLLGQKVSQILISGV 61  
QY 85 TSNDRGKVGKNKAYLERWLTSIPPLFAGESVFQINFQWD--ENFGFPGAFFIKNGHTSEFF 143  
Db 62 NYDGLGKLSNPAYLESWLTDTITAGESTSVTFDWRDDEFQVGPVAFIKNLHNEFF 121  
QY 144 LKSLTLDVPGYGRVHFDGNSWVPSGRYKDKRIFFAHNVYLPSTQNPRLKRYREELWN 203  
Db 122 LKSLTLEDVPNYKIHFCVNSWVPAFRYKSDRIFFANQAYLPSETPQPLRKYRENELVA 181  
QY 204 LRGGDTGERKEWDRIYDVYNDIADPDVGDH--RPILGGTTEYPYPRRGTRGRPSRRD 261  
Db 182 LRGGDTGKLEWDVYACVNDLGECDKGEYARPIILGSSSEYFYPFRGRTGREPTKAD 241  
QY 262 HNYESRSLPMSLDIYVPKDNFGLKVDPLGLVTLKALISIKPGLQSFIDVTPNEFDN 321  
Db 242 PNCESRNPLMSLDIYVPRDRFRGHVKKSDPLTSSLSLQTLPLFAKALCDNTNEFNS 301

```
QY 322 FKEVNLFRGPPIPFNAF-KTLEDELDLPPFLKALVRNDGKFLKFTTPEVVKDKIGWS 380
DB 302 FADVLNLYEGGIKPEGPWLKAITDNISSEILKDIQTDGGLKYTPQVQIGDKTAWR 361
QY 381 TDEEFAREMLAGNPLLRLEAPPTSKLDPNVYGNQNSITTEEHKKGHGDGLTVDKAM 440
DB 362 TDEEFAREMLAGNPLLRLEAPPTSKLDPNVYGNQNSITTEEHKKGHGDGLTVDKAM 421
QY 441 KQNRLLIYVDPHDALPMLYLRN-ATSTKYATRTLLKDDGTLKPLVIELALPHPOGDQ 499
DB 422 KSNRLFILNHHIDIVMPLLRKIMGSAANTKAYASRTLLFLQDDRTLLKPLAIELSLPHPDQ 481
QY 500 LGATSKLYFPAENGVOKSIWOLAKAYVTVNDGVHQLISHWLHVALEPFIATHRQLS 559
DB 482 FGTYSKVYTPADQGVESIGWQFAKAYAVNDMGHQLISHWLHVALEPFIATHRQLS 541
QY 560 VILPHIKLLVPHYKDTMFINASARQVLINANGLIETTHYPSKYSMESSILYKDWTPPDQ 619
DB 542 VILPHIKLLVPHYKDTMFINASARQVLINANGLIETTHYPSKYSMESSILYKDWTPPDQ 600
QY 620 ALPNMLKRGGLAVEDSSAPHGRLILLNDYPYAVDGLDIWSAIIKTVQDCLYKDDNAV 679
DB 601 ALPADLLKRGGLAVEDSSAPHGRLILLNDYPYAVDGLDIWSAIIKTVQDCLYKDDNAV 660
QY 680 QNDPELQSWNRELKREKGHADKKEHPMPKMTLSLSELIESCTTIIWIASALHAAVNFQY 739
DB 661 EKDTELOQWKLREKREKGHADKKEHPMPKMTLSLSELIESCTTIIWIASALHAAVNFQY 720
QY 740 YGGYILNRPPTTSRRMPVEGTAAYKELESNPEKAFRLTICSELQALYSIIIEILSKHAS 799
DB 721 YAGYILNRPPTTSRRMPVEGTAAYKELESNPEKAFRLTICSELQALYSIIIEILSKHAS 780
QY 800 DEVILGQASDWTSDKTALAEFAKFGKQLFEVENRIMERKEVNLKNSRGPVNLPTLL 859
DB 781 DEVILGQASDWTSDKTALAEFAKFGKQLFEVENRIMERKEVNLKNSRGPVNLPTLL 840
QY 860 VPSSNEGTLGRGPNISISI 878
DB 841 FPTSBEGLTGKGNPSVSI 859

RESULT 9
S01864
lipoxigenase (EC 1.13.11.12) 3 - soybean
C:Species: Glycine max (soybean)
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 28-Apr-1993
C:Accession: S01864
R:Yenofsky, R.L.; Pine, M.; Liu, C.
Mol. Gen. Genet. 211, 215-222, 1988
A:Title: Isolation and characterization of a soybean (Glycine max) lipoxigenase-3 gene.
A:Reference number: S01864
A:Accession: S01864
A:Molecule type: mRNA
A:Residues: 1-857 <YEN>
A:Cross-references: EMBL:X06928
C:Genetics:
A:Gene: lox-3
A:Introns: 70/1; 165/3; 246/1; 353/1; 381/3; 417/3; 519/2; 607/2
C:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match 59.4%; Score 2776; DB 2; Length 857;
Best Local Similarity 60.1%; Pred. No. 3.7e-181;
Matches 522; Conservative 132; Mismatches 183; Indels 32; Gaps 7;

QY 28 GNILDRVSSLGCKIKGKVIILMRNVLDFTFEHS-----NLLDNFTLGGG 74
DB 3 GGLLH-----GHKIKGTVLMRKNVLDVNSVTSVGGIIGQLDLVGSITDLTATFLGRP 57
QY 75 VSPQLISATHNSDRSGKGVGNKAYLERWLTISIPPLFAGESVQINFQWDFGPGAFFI 134
DB 58 VSLQLISATKADANGKGLKATFLEGIITSLPTLGAGQAFKINFEDWDGSGILGAFYI 117
```

```
QY 135 KNGHTSEFFLSKLTLDVPGYGRVHFDNCNWPYSGRYKKDIRIFFANHVIYLPSTPNPLR 194
DB 118 KNFMQTEFFLVSLTLEDIPNHSIHVFCNSWYINAKLFKSDRIFFANQTYLPSETPAVLV 177
QY 195 KYREBELNLRGDCGERKEWDRIYDYNVDIADPDVDGH--RPILGGTTEYVPRGR 252
DB 178 KYREBELNLRGDCGERKEWDRIYDYNVDIADPDVDGH--RPILGGTTEYVPRGR 237
QY 253 TGRPSRRDRHNYESRLSPIMSLDIYVPKDNFGLHMSDFLGYTLKALSISIKFQLOQIF 312
DB 238 TGRKPTRKDPNSES-----SNDVYLPDEAFGLHKSDFLTYGLKSVSQNVLPLOQAF 292
QY 313 DV--TPNEFDFRKYVDNLFPERGFPIPFNAFKLTLEDLP-PLFKALVRNDGKELKFPPT 369
DB 293 DLNFTPREFDSFDEVHGLYSGGIKLPTD-----ISKISPLVLEKIFFTDGEQALKFPPT 348
QY 370 EYVKONKIGWSTDEBFAREMLAGNPLLRLEAPPTSKLDPNVYGNQNSITTEEHKH 429
DB 349 KVIQVSKSAWMTDEBFAREMLAGNPNLIRCLKRPFPKSKLDSQVYGDHTSQITKEHLEP 408
QY 430 GUDGLTVDEAMKQNRLLYVDPHDALPMLYLRNATSTKYATRTLLKDDGTLKPLVIE 489
DB 409 NLEGLTVDEAIQNKSLFLGLGHDPIMPYLRINATSTKAYATRTILFLKNDGTLRPLAIE 468
QY 490 LALPHQGDQLGALSKLYFPAENGVOKSIWOLAKAYVTVNDGVHQLISHWLHVALEP 549
DB 469 LSLPHQGDQSGAPSOVFLPADEGVESIIWOLAKAYVTVNDGVHQLISHWLHVALEP 528
QY 550 FVIATHROLVSLPHIKLLVPHYKDTMFINASARQVLINANGLIETTHYPSKYSMESS 609
DB 529 FFIATNRHLSVHPIYKLLHYRDTMNGIARLSLVNDGGVTEQTLWGRYSVMSAV 588
QY 610 LYKDWTFDQALPNMLKRGGLAVEDSSAPHGRLILLNDYPYAVDGLDIWSAIIKTVQD 669
DB 589 VTKDWTFDQALPADLIRGMAIEDPSCPHGRLVIEDYPYAVDGLDIWSAIIKTVQD 648
QY 670 CLYKDDNAVQNDPELQSWNRELKREKGHADKKEHPMPKMTLSLSELIESCTTIIWIASAL 729
DB 649 FLYKSDDTLREDBELQACWELVEVGHGDKKPEKMPKMTREELVEACAIITWASAL 708
QY 730 HAAVNFQYVGGYILNRPPTTSRRMPVEGTAAYKELESNPEKAFRLTICSELQALYS 789
DB 709 HAAVNFQYVGGYILNRPPTTSRRMPVEGTAAYKELESNPEKAFRLTICSELQALYS 768
QY 790 IIEILSKHASDEVILGQASDWTSDKTALAEFAKFGKQLFEVENRIMERKEVNLKNSR 849
DB 769 VIEILSKHASDEVILGQASDWTSDKTALAEFAKFGKQLFEVENRIMERKEVNLKNSR 828
QY 850 GPVNLPTLLVPSSNEGTLGRGPNISISI 878
DB 829 GPVNLPTLLVPSSNEGTLGRGPNISISI 857

RESULT 10
S07075
lipoxigenase (EC 1.13.11.12) 2 [similarity] - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: S07075
R:Bailey, P.M.; Casey, R.
Biochem. J. 264, 929-932, 1989
A:Title: The cDNA cloning of a pea (Pisum sativum) seed lipoxigenase. Sequence comparison
A:Reference number: S07075; M01D:90147555; PMID:2515855
A:Accession: S07075
A:Molecule type: mRNA
A:Residues: 1-864 <EAL>
A:Cross-references: EMBL:X17061; NID:G20801; PIDN:CAA34906.1; PID:G20802
C:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match 57.9%; Score 2705.5; DB 1; Length 864;
Best Local Similarity 59.9%; Pred. No. 2.4e-176;
```



Db 848 PYMLLPNAGSDNSBSGLTGKIPNSVSI 876  
RESULT 12  
S01142  
lipoxxygenase (EC 1.13.11.12) 3 [similarity] - garden pea  
C:Species: Pisum sativum (garden pea)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: S01142  
R:Ealing, P.M.; Casey, R.  
Biochem. J. 253, 915-918, 1988  
A:Title: The complete amino acid sequence of a pea (Pisum sativum) seed lipoxxygenase protein  
A:Reference number: S01142; MUID:89025643; PMID:3140791  
A:Accession: S01142  
A:Molecule type: mRNA  
A:Residues: 1-861 <EAL>  
A:Cross-references: EMBL:X07807; NID:g20799; PIDN:CAA30666.1; PID:g20800  
C:Superfamily: lipoxxygenase  
C:Keywords: oxidoreductase  
Query Match 57.7%; Score 2696.5; DB 1; Length 861;  
Best Local Similarity 58.3%; Pred. No. 9.8e-176;  
Matches 506; Conservative 145; Mismatches 184; Indels 33; Gaps 7;  
QY 30 ILDRVSSLGKNGKIKGVLMNSVLDFT-----EFHSLNDNFTLLGGGVS 76  
Db 8 ILNR-----GHKIKGVLMNRKVLNLSLTVGVGQGFIDLGSTVDNLTAFLGRSV 62  
QY 77 FQLISATHTSNDNRKGVNGKAYLERWLTSLIPPLFAGESVFOINPQWENFGFGAFPIKN 136  
Db 63 LQLISATKPDATGKGLKATFLEGIISSLTPLGAGOSAPKIHFEWDDMGIPAFYIKN 122  
QY 137 GHTSEFFLKSLLDVPYGRVHDFCSNWYPSGRYKDRFFANHYVLSQTPNPKRY 196  
Db 123 FMTQTEFFLVSLDIDPHNGSIYFCVNSWIYNAKHKKIDRFANQYLYLSETPAPLVHY 182  
QY 197 REELNLNRDGTGRKEWDRIYDVYNDIADPDVGDH--RPLIGGTETPYPPRRGRGT 254  
Db 193 REELNLNRDGTGRKEWRIYDVYNDIADPDVGDH--RPLIGGTETPYPPRRGRGT 242  
QY 255 RPRSRDNRYSRLSPINSLDIYVPKDNFGHLKQSDPLGLYTLKALISIKPLQSI-- 312  
Db 243 RKPTRKDNSESR-----SDYVYLPDRFAFGHLKSSDFLYGLKAVSQNVVPALESVFFD 297  
QY 313 -DVTPEFNDNFKEVDNLPFERGPIPENAFKTLTDLTP-PLFKALVRNDGKELKPTPE 370  
Db 298 LNFTPEFDSFDEHGLYEGGIKLPN-----ILSQISPLPVKLEIFTDGENTLYKPPPK 353  
QY 371 VYKDNKIOWSTDEBFARMLAGNPLLRLEAPPTSKLDPNVYGNQNSTITEEHKHG 430  
Db 354 VIQVSRSGWMTDESFARMLAGVNPVICCLQEPFPRSKLDSQIYGDHTSKISKEHLEPN 413  
QY 431 LDGLTVDEAMKONRLIYVDFDALMPYLTMRNATSTKYATRLTLKLLKDDGTGKPLVIEL 490  
Db 414 LEGLTVEAIGKQLLDHDSIMPLYRRLNSTKAYATRLTLFLNNQNLKPLAIEL 473  
QY 491 ALPHPQGGQOLGAIKLYPPAENGQKSTIWLAKAYVTVNDVGHQLISHMLHVALEPP 550  
Db 474 SLPHPQGGDEGAVSVYQPALGEVSSIWLAKAYVTVNDVGHQLISHMLHVALEPP 533  
QY 551 VIATHRQLSVLPHPTKLLVPHYKDTMTINASARQVLNANGLIETHYPKYSNWEISSIL 610  
Db 534 VIATNRHLSCUHPYKGLYPHYRDTMINSARLSLVNDGGIETKFTLWGRYSNEMSSKV 593  
QY 611 YKDTFFPQALPNMLKRGGLAVESDSSPHGLRLRLINDYPPAVDGLDTSWAIKTVQDYCC 670  
Db 594 YKNWVFTQALPADLIRKGMALDESPSPCGVKLVVEDYPPAVDGLLEWAIKTVQDYVS 653  
QY 671 LYYKDDNAVQNDPELOSWNLEKRGHAKKHGEPWPMQNTLSELIESCTTIWIASALH 730  
Db 654 LYYSDEKILQDSLOQAWKELVGVGDKKNEPMPKMTREDLIEVCISIVTWSALH 713  
QY 731 AAVNFGQPYGGYILNRPTTSRRFMPVEGTAEBYKELESNPKEAFRLTICSLQALVSI 790

Db 714 AAVNFGQSYGGLILNRPTLSRRFMPKGSABFEELVKSQKAYLTKTPKFQTLIDLVS 773  
QY 791 IEILSKHASDEVYLGORASIDWTSKIALERPEKFGKNLFVEVIMERNKEVNLKNSG 850  
Db 774 IEILSRHASDEYLGORONPNWTSKRALAPKFGKNLAIEKKLTQRNNDKURNRHG 833  
QY 851 PYNLPYTLVPSNNEGLTGRGIPNSISI 878  
Db 834 PYEMPYTLVPSKKEGLTFRGIPNSISI 861  
RESULT 13  
DASYLI  
lipoxxygenase (EC 1.13.11.12) 2 - soybean  
N:Alternate names: carotene oxidase 2; lipoxidase 2  
C:Species: Glycine max (soybean)  
C:Date: 31-Mar-1989 #sequence\_revision 30-Jun-1991 #text\_change 19-Jan-2001  
C:Accession: A28161; A30831; A37160; S13536  
R:Shibata, D.; Steczko, J.; Dixon, J.E.; Andrews, P.C.; Hermodson, M.; Axelrod, B.  
J. Biol. Chem. 263, 6816-6821, 1988  
A:Title: Primary structure of soybean lipoxxygenase L-2.  
A:Reference number: A28161; MUID:88198254; PMID:2834391  
A:Accession: A28161  
A:Molecule type: mRNA  
A:Residues: 1-865 <SHI>  
A:Cross-references: GB:J03211; NID:gl70013; PIDN:AAA33987.1; PID:gl70014  
A:Note: there are no disulfide bonds  
R:Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.  
Plant Mol. Biol. 7, 11-23, 1986  
A:Title: Two soybean seed lipoxxygenase nulls accumulate reduced levels of lipoxxygenase  
A:Reference number: A30831  
A:Accession: A30831  
A:Molecule type: mRNA  
A:Residues: 232-262, 'NL', 265-312, 'Y', 314-362, 'E', 364-399, 'P', 401-427, 'H', 429-485, 'G', 487  
A:Cross-references: GB:M16876  
A:Experimental source: clone PLX-65  
A:Note: due to a frameshift error, residues in the region 691-865 do not correspond to  
R:Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.  
unpublished results, cited by Yenofsky, R.L., Fine, M., and Liu, C., in Mol. Gen. Genet.  
A:Reference number: A37160  
A:Accession: A37160  
A:Molecule type: mRNA  
A:Residues: 232-312, 'Y', 314-399, 'PK', 402-427, 'H', 429-485, 'G', 487-501, 'G', 50  
A:Note: this is a revision to the sequence from reference A30831  
R:Shibata, D.; Kato, T.; Tanaka, K.  
Plant Mol. Biol. 16, 353-359, 1991  
A:Title: Nucleotide sequences of a soybean lipoxxygenase gene and the short intergenic re  
A:Reference number: S13381; MUID:91370880; PMID:1909908  
A:Accession: S13536  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 859-865 <SH2>  
A:Cross-references: EMBL:X56139; NID:gl8745; PIDN:CAA33605.1; PID:g829267  
C:Comment: In soybean, four isozymes are found with distinct electrophoretic properties.  
C:Function:  
A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis pen  
C:Superfamily: lipoxxygenase  
C:Keywords: fatty acid oxidation; iron: metalloprotein; oxidoreductase  
F:527,532,718,722,865/Binding site: iron (His, His, His, Asn, Ile) #status predicted  
Query Match 57.5%; Score 2690; DB 1; Length 865;  
Best Local Similarity 58.4%; Pred. No. 2.8e-175;  
Matches 513; Conservative 127; Mismatches 194; Indels 44; Gaps 8;  
QY 23 VTNAGNILDVSSVGGNKGKIVLMNSVLDFTTEFH-----SNLL 64  
Db 10 ILNR-----GGHKIKGVLMNRKVLNLSLTVGVGQGFIDLGSTLVNVGSL 59  
QY 65 DNFTLGGGVFSQLISATHTSNDNRKGVNGKAYLERWLTSLIPPLFAGESVFOINPQW 124  
Db 60 DNLTAFLGRVALQLISATKPLANGKGVKGTDFLEGIIVSLPTLGAGESAFNIQFWE 119



R:Bunker, T.W.; Koetje, D.S.; Stephenson, L.C.; Creelman, R.A.; Mullet, J.E.; Grimes, H.  
 Plant Cell 7, 1319-1331, 1995  
 A:Title: Sink limitation induces the expression of multiple soybean vegetative lipoxigenase  
 A:Reference number: Z15673; MUID:96004535; PMID:7549487  
 A:Accession: T06429  
 A>Status: Preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-859 <BUN>  
 A:Cross-references: EMBL:U26457; NID:G1262439; PIDN:AAA96817.1; PID:G1262440  
 A:Experimental source: cultivar Wye; leaf  
 C:Genetics:  
 A:Gene: vlxc  
 C:Function:  
 A:Description: catalyzes hydroperoxidation of polyunsaturated fatty acids containing a  
 C:Superfamily: lipoxigenase  
 C:Keywords: iron; metalloprotein; oxidoreductase

Query Match 56.7%; Score 2649; DB 2; Length 859;  
 Best Local Similarity 58.0%; Pred. No. 1.7e-172; Mismatches 187; Indels 44; Gaps 8;  
 Matches 503; Conservative 133; Mismatches 187; Indels 44; Gaps 8;

QY 39 GNKIKGVILMSNYLDFTEPHS-----NLLDNFTTELLGG-----VS 76  
 Db 10 GQKIKGTVVLMPKNDLNAITSVKGSGAKDTATDFLGKGLDALGHAVALTAFAGHSIS 69  
 QY 77 FQLISATHSNDNRGKGVKNAYLEWLTISIPFAGESVQFQINQWENRGFGCAFIKN 136  
 Db 70 LQLISATQTDGSGKGVKNAYLEKFLTPTLARGAQAFDINFWDASFGIPGAFYIKN 129  
 QY 137 GHTSEFFLKSLTDVPVGYGRVHFPCNSWYPSGKDRIFFAHNVLPSPQENPLRKY 196  
 Db 130 FMTDFEFLVSKLEDPNEGIFNVCSWVNFKSKYKKNRIFVNDYVLPSTFGLVY 189  
 QY 197 REEELWNI RGDTGKERKWDRIYDVYNDADPDVGDHRLPILGTTETYPYPRGRTRGP 256  
 Db 190 RQEELEVLRGDTGKRRDFRIYDIYNDLGNPDGDPRIIGSSNYPYPRVRTGRE 249  
 QY 257 RSRDRHNVESRLSPIMSIDIYVPKDNFGLKMSDFLGYTLKALSISIKPGLOSI---FD 313  
 Db 250 KTRKDPNSEK-----PGEIYVPRDENFGLKSSDFLTGYIKSLSONVPLFKSIIILNR 303  
 QY 314 VTPNFDNPKVDNLFERGFPIPNFAKTLTDLTP-PLFKALVRNDGEXFLKPPPTPEVY 372  
 Db 304 VTSSEFDSFDEVRGUFEGGKILPTN-----ILSQISPLPLVKEIFRTDGTENTLQPPPHVI 359  
 QY 373 KDNKIGWSTDEFAFEMLAGNPILLIRELEAPPTSKLDPNVYGNQNSTITEHKKGLD 432  
 Db 360 RVSKSGWMTDEFAKEMTAGVNPVIRLQEPFPKSLDPAITYGDTSTITKQOLEINLG 419  
 QY 433 GLTVDEAMKQRLXIVDFHDALMPYLTRMNAIS-TKTYATRTLLLLKDDGTLKPLVIELA 491  
 Db 420 GVTVEEALSAHRLFLDYHDFAFFPYLTAKINSLPIAKAYATRTILFKDDGSLKPLAIELS 479  
 QY 492 LPHPGQDQGLGAIKLYPFAENGQVKSIMOLAKAYVTVNDVGHQIISHNLHVALEPFV 551  
 Db 480 KP-----ATVSKVLPATGEVVESTIWLAKAHVIVNDSGYHQLISHNLNTHAVMEPPA 532  
 QY 552 IATHRLQSLVLPVHKLVLPHYKDTMFMFNASARQVLINANGLIETTHYPKYSMELSSILY 611  
 Db 533 IATNRLHSLVLPVYKLLVPHYKDTININGLARQSLINAGGIIETFLPGKYSIEMSSVY 592  
 QY 612 KQWTFPDQALPNLMKRGIAVEDSAPHGLRLINDYPPFAVDGLDIWSAIAKTWVQDYCCL 671  
 Db 593 KXWVFTDQALPADLVKRGIAVEDSAPHGLRLVIEDYPYAVDGLIWDIAIKTWVHEYVS 652  
 QY 672 YYKDDNAVQNDPELQSWNNEUREKHADKKHPPWPKMQLSELIESCCTIIIIWASALHA 731  
 Db 653 YYPINAAIQQDTELAQAWKEVVEKGGHGLDKKPPWPKLQTVEDLIQSCSIIIIWASALHA 712  
 QY 732 AVNFGQYPIGYIILNRPITSRFMPVEVGTABYKELESNPKAFURITICSELQALVSIISII 791  
 Db 713 AVNFGQYPIGYIIVNRPITLARRFIFEEGTKEYDEMVKDPQKAYLRTITPKFETLIDISVI 772

QY 792 EILSKHASDEVYLGQRASIDWTSKIALEAFKFGKLFQKLFVEVNRIMERKEVNLKNRSGP 851  
 Db 773 EILSRHASDEVYLGQRDNPNWTTDSKALEAFKFGKLFQKLFVEVNRIMERKEVNLKNRSGP 832  
 QY 852 VNLPTYLLVPSSNEGILTRGIENSI 878  
 Db 833 VQLPYTLHRSSEEGMSFKGIENSI 859

Search completed: July 16, 2004, 12:03:55  
 Job time : 43.0332 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2004, 11:30:53 ; Search time 167.411 Seconds  
(without alignments)  
1481.839 Million cell updates/sec

Title: US-09-937-908-1

Perfect score: 4675  
Sequence: 1 MFGIGKNIIEGALNTTGDLA.....LVPSSNEGLTGRGIPNSISI 878

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_29Jan04.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4675	100.0	878	4 AAB11500	C. sativu
2	4575	100.0	878	4 AAB86036	Cucumber
3	3933	84.1	880	6 AAO27492	Balsam pe
4	3011.5	64.4	859	6 ABO19443	Wine grap
5	2995.5	64.1	862	6 ABO19442	Wine grap
6	2992.5	64.0	857	4 AAB46803	Potato LO
7	2911	62.3	862	6 ABO19404	Amino aci
8	2791	59.7	857	5 ABO30570	Glycine m
9	2690	57.5	865	5 ABO30569	Glycine m
10	2639.5	56.5	864	2 AAR24042	Lipoxigen
11	2591	55.4	853	2 AAR50220	Soybean l
12	2582.5	55.2	839	5 ABO30568	Glycine m
13	2502	53.5	863	7 ADC53139	9'-specif
14	2439.5	52.2	837	6 ADA48504	Rice prot
15	2438	52.1	862	5 AAU99691	Barley wi
16	2438	52.0	862	5 ABO30566	Wild type
17	2431	52.0	862	5 AAU99693	Barley wi
18	2431	52.0	862	5 AAU99692	Barley wi
19	2431	52.0	862	5 ABO30567	Mutant ty
20	2424	51.9	864	5 ABO30571	Barley lo
21	2423.5	51.8	887	6 AAO27494	Corn (Zea
22	2390.5	51.1	865	2 AAR23797	Rice lipo
23	2390.5	51.1	865	2 AAR20670	Lipoxigen
24	1845	39.5	491	7 AAE39891	Human lip
25	1705.5	36.5	924	6 AAE38266	Rice dise

26	1656	35.4	923	2 AAR61136	Aar61136 Plant bli
27	1653	35.4	901	4 AAY97741	Aay97741 H. annus
28	1628	34.8	445	6 AAO27493	Aao27493 Garden ba
29	1498.5	32.1	922	5 AAU76150	Aau76150 Rice lipo
30	1316	28.1	244	4 AAB86035	Aab86035 Cucumber
31	790	16.9	301	3 AAG24811	Aag24811 Arabidops
32	773.5	16.5	464	6 AAO27495	Aao27495 Corn (Zea
33	722	15.4	312	3 AAG23228	Aag23228 Arabidops
34	706.5	15.1	222	4 AAG83338	Aag83338 P patens
35	706.5	15.1	222	4 AAG80888	Aag80888 Lipid deg
36	674.5	14.4	170	6 AAO27487	Aao27487 Balsam pe
37	552	11.8	240	3 AAG23230	Aag23230 Arabidops
38	546.5	11.7	193	3 AAG24812	Aag24812 Arabidops
39	546.5	11.7	242	3 AAG23229	Aag23229 Arabidops
40	516.5	11.0	663	5 AAE15433	Aae15433 Human 5-1
41	516.5	11.0	674	1 AAP90730	Aap90730 Synthetic
42	516.5	11.0	674	5 AAE15432	Aae15432 Human 5-1
43	516.5	11.0	674	6 ABU08713	Abu08713 Alzheimer
44	516.5	11.0	674	6 ABU89732	Abu89732 Protein d
45	516.5	11.0	674	6 ABR42216	AbR42216 Mouse CAS

#### ALIGNMENTS

#### RESULT 1

AAB11500  
ID AAB11500 standard; protein; 878 AA.

XX AAC11500;

DT 13-MAR-2001 (first entry)

XX C. sativu LOX protein.

DE C. sativu LOX protein.

XX LOX; lipoxigenase; cucumber; plant; 6-hydroperoxy-gamma-linolenic acid;

KW 9-hydroperoxy-gamma-linolenic acid; 6,9-hydroperoxy-gamma-linolenic acid;  
KW gamma-linolenic acid.

XX Cucumis sativus.

XX DE19914464-AL.

XX 05-OCT-2000.

XX 30-MAR-1999; 99DB-01014464.

XX 30-MAR-1999; 99DB-01014464.

XX (IPBP-) IPB INST PFLANZENBIOCHEMIE.

XX Feussner I, Hornung E;

XX WPI; 2001-103874/12.

XX Preparation of plant lipoxigenase with altered position specificity

XX comprises replacing at least one amino acid in the wild type lipoxigenase

XX amino acid sequence.

XX Disclosure; Fig 5; 14pp; German.

XX This invention describes a novel preparation of plant lipoxigenase (I)

XX with altered position specificity which comprises replacing at least 1

XX amino acid in the wild type lipoxigenase amino acid sequence. The method

XX also describes (1) (1) prepared by the method above; (2) nucleic acid

XX encoding (1); (3) a vector comprising the nucleic acid of (2); (4) a cell

XX comprising the vector of (3); (5) a plant or plant part comprising a host

XX cell as in (4); (6) preparation of 6-, 9- and/or 6,9-hydroperoxy-gamma-

XX linolenic acid comprising reacting gamma-linolenic acid with (1); and (7)

XX a gamma-linolenic acid derivative comprising a hydroperoxy group or a

XX hydroxy group at position 6

XX Sequence 878 AA;

```
Query Match      100.0%; Score 4675; DB 4; Length 878;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

.QY 1 MFGIGKNIIEGALNTTGLAGSVINAGNILDVSSLGKNIKGKVIILMRNSVLDFTTEFH 60
    |||
Db 1 MFGIGKNIIEGALNTTGLAGSVINAGNILDVSSLGKNIKGKVIILMRNSVLDFTTEFH 60
    |||

.QY 61 SNLLDNFTLLGGGVSFOLISATHTSNDGRGVGNKAYLERWLTSPPLFAGESVFQINF 120
    |||
Db 61 SNLLDNFTLLGGGVSFOLISATHTSNDGRGVGNKAYLERWLTSPPLFAGESVFQINF 120
    |||

.QY 121 QNDENFGPGAFPIKNGHTSEFFLKSLLTDDVPGYGRVHFDNCNSWVYSGYKDRIFFA 180
    |||
Db 121 QNDENFGPGAFPIKNGHTSEFFLKSLLTDDVPGYGRVHFDNCNSWVYSGYKDRIFFA 180
    |||

.QY 181 NHVYLPSTPNPLRYREELNWLNGDGTGERKEWDRIYDYVDVNDIADPDVGDHRPILG 240
    |||
Db 181 NHVYLPSTPNPLRYREELNWLNGDGTGERKEWDRIYDYVDVNDIADPDVGDHRPILG 240
    |||

.QY 241 GTTEYPYPRRGTRGPRSRDHNYESRLSPIMSLDIYVPKDNFCHLKMDFLGYTLKAL 300
    |||
Db 241 GTTEYPYPRRGTRGPRSRDHNYESRLSPIMSLDIYVPKDNFCHLKMDFLGYTLKAL 300
    |||

.QY 301 SISIKPGLQSIQIDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTEDLTPPLFKALVRNDG 360
    |||
Db 301 SISIKPGLQSIQIDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTEDLTPPLFKALVRNDG 360
    |||

.QY 361 EKFLKFPPEVVKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420
    |||
Db 361 EKFLKFPPEVVKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420
    |||

.QY 421 TITEEHIKHGLDGLTVDEAMKQNRLYIVDFHDLMPYLTRMNAVSTKTYATRTLLLLKDD 480
    |||
Db 421 TITEEHIKHGLDGLTVDEAMKQNRLYIVDFHDLMPYLTRMNAVSTKTYATRTLLLLKDD 480
    |||

.QY 481 GTLKPLVIELALPHQGGQOLGAIKLYPFAENGQVKSILQAKAYVTVDVGHOLISHW 540
    |||
Db 481 GTLKPLVIELALPHQGGQOLGAIKLYPFAENGQVKSILQAKAYVTVDVGHOLISHW 540
    |||

.QY 541 LHTHAVLEPFFVIATHRQLSVLHPHKLAVPHYKDTMFINASARQVLINANGLIBETHYPS 600
    |||
Db 541 LHTHAVLEPFFVIATHRQLSVLHPHKLAVPHYKDTMFINASARQVLINANGLIBETHYPS 600
    |||

.QY 601 KYSMELSSILYKDWTFPQOALPNNLMKGLAVERSSAPHGRLILINDYPPAVDGLDWSA 660
    |||
Db 601 KYSMELSSILYKDWTFPQOALPNNLMKGLAVERSSAPHGRLILINDYPPAVDGLDWSA 660
    |||

.QY 661 IKTWYQDYCCLYYKDDNAVQNDFELQSWWNELEKRGHADKKHEPWPWKMTLSLIESCT 720
    |||
Db 661 IKTWYQDYCCLYYKDDNAVQNDFELQSWWNELEKRGHADKKHEPWPWKMTLSLIESCT 720
    |||

.QY 721 TIWIASALHAANFGQPYGGYILNRPRTTSRRPMPVEGTAIEYKELSNPEKAPLRTICS 780
    |||
Db 721 TIWIASALHAANFGQPYGGYILNRPRTTSRRPMPVEGTAIEYKELSNPEKAPLRTICS 780
    |||

.QY 781 ELQALVSIISIIELSKHASDEVILGORASIDWTSKIALAEFAFEFGKQLFEVENRIMERN 840
    |||
Db 781 ELQALVSIISIIELSKHASDEVILGORASIDWTSKIALAEFAFEFGKQLFEVENRIMERN 840
    |||

.QY 841 KEVNLKNSGPNVLPYTLVPSNNEGLTGRGIPNSISI 878
    |||
Db 841 KEVNLKNSGPNVLPYTLVPSNNEGLTGRGIPNSISI 878
    |||

RESULT 2
AAB86036
ID AAB86036 standard; protein; 878 AA.
XX
AC AAB86036;
XX
DT 13-JUL-2001 (first entry)
```

```
XX DE Cucurbit LBLOX protein SEQ ID 4.
XX KW Cucurbit; LBLOX; fatty acid metabolism; lipid metabolism;
XX KW plant oil-production; transgenic plant.
XX OS Cucumis sativus.
XX PN DE19950921-A1.
XX PD 26-APR-2001.
XX PF 21-OCT-1999; 99DE-01050921.
XX PR 21-OCT-1999; 99DE-01050921.
XX PA (BADI ) BASF AG.
XX PI Kindl H, May C, Feussner I;
XX DR WPI; 2001-274658/29.
XX DR N-PSDB; AAF88022.
XX PT New isolated nucleic acid encoding sequence that targets proteins to
XX PT lipid bodies, useful for producing transgenic plants for lipid and fatty
XX PS acid production.
XX PS Disclosure; Page 18-21; 30pp; German.
XX CC This invention describes a novel isolated nucleic acid sequence (I),
XX CC encoding a polypeptide, comprising a sequence (Ia) involved in fatty acid
XX CC or lipid metabolism, and a targeting sequence (Ib). (I) are used to
XX CC produce oil-producing transgenic plants or eukaryotic microorganisms, for
XX CC production of lipids or derived fatty acids. This sequence represents a
XX CC Cucumis sativus (cucumber) LBLOX protein which is described in the method
XX CC of the invention
XX SQ Sequence 878 AA;

Query Match      100.0%; Score 4675; DB 4; Length 878;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

.QY 1 MFGIGKNIIEGALNTTGLAGSVINAGNILDVSSLGKNIKGKVIILMRNSVLDFTTEFH 60
    |||
Db 1 MFGIGKNIIEGALNTTGLAGSVINAGNILDVSSLGKNIKGKVIILMRNSVLDFTTEFH 60
    |||

.QY 61 SNLLDNFTLLGGGVSFOLISATHTSNDGRGVGNKAYLERWLTSPPLFAGESVFQINF 120
    |||
Db 61 SNLLDNFTLLGGGVSFOLISATHTSNDGRGVGNKAYLERWLTSPPLFAGESVFQINF 120
    |||

.QY 121 QNDENFGPGAFPIKNGHTSEFFLKSLLTDDVPGYGRVHFDNCNSWVYSGYKDRIFFA 180
    |||
Db 121 QNDENFGPGAFPIKNGHTSEFFLKSLLTDDVPGYGRVHFDNCNSWVYSGYKDRIFFA 180
    |||

.QY 181 NHVYLPSTPNPLRYREELNWLNGDGTGERKEWDRIYDYVDVNDIADPDVGDHRPILG 240
    |||
Db 181 NHVYLPSTPNPLRYREELNWLNGDGTGERKEWDRIYDYVDVNDIADPDVGDHRPILG 240
    |||

.QY 241 GTTEYPYPRRGTRGPRSRDHNYESRLSPIMSLDIYVPKDNFCHLKMDFLGYTLKAL 300
    |||
Db 241 GTTEYPYPRRGTRGPRSRDHNYESRLSPIMSLDIYVPKDNFCHLKMDFLGYTLKAL 300
    |||

.QY 301 SISIKPGLQSIQIDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTEDLTPPLFKALVRNDG 360
    |||
Db 301 SISIKPGLQSIQIDVTPNEFDNFKEVDNLFERGFPIPFNAFKLTEDLTPPLFKALVRNDG 360
    |||

.QY 361 EKFLKFPPEVVKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420
    |||
Db 361 EKFLKFPPEVVKONKIGWSTDESFAREMLAGNPLIRLEAPPTSKLDPNVYGNQNS 420
    |||

.QY 421 TITEEHIKHGLDGLTVDEAMKQNRLYIVDFHDLMPYLTRMNAVSTKTYATRTLLLLKDD 480
    |||
Db 421 TITEEHIKHGLDGLTVDEAMKQNRLYIVDFHDLMPYLTRMNAVSTKTYATRTLLLLKDD 480
    |||
```

Db 421 TITEHINKHGLDGLTVDEAMKQNLXYVDFHDLMPYLTRMNATSTKYATRILLKDD 480  
 Qy 481 GTLKPLVIELALPHPQGDQLGALSKLYFPAENGQVQKSIWOLAKAYTVNDVGYHQLISHW 540  
 Db 481 GTLKPLVIELALPHPQGDQLGALSKLYFPAENGQVQKSIWOLAKAYTVNDVGYHQLISHW 540  
 Qy 541 LHTHAVLEPPFVIATHRQLSVLHPHKLIVPHYKDTMETINASARQVLINANGLIETHYPS 600  
 Db 541 LHTHAVLEPPFVIATHRQLSVLHPHKLIVPHYKDTMETINASARQVLINANGLIETHYPS 600  
 Qy 601 KYSMELSSILYKDWTFDQALPNNLMKRGGLAVEDSSAPHGRLRLINDYPFAVDGLDIWSA 660  
 Db 601 KYSMELSSILYKDWTFDQALPNNLMKRGGLAVEDSSAPHGRLRLINDYPFAVDGLDIWSA 660  
 Qy 661 IKTWQDYCCLYYKDDNAVQNDPHELOSWNLEKGHADKXHEPWPMPQOTLSELBSCT 720  
 Db 661 IKTWQDYCCLYYKDDNAVQNDPHELOSWNLEKGHADKXHEPWPMPQOTLSELBSCT 720  
 Qy 721 TIWIASALHAANVFGQYPYGGYILNRPFTTSRRPMPVEGTAAYKELESNPEKAFRLTICS 780  
 Db 721 TIWIASALHAANVFGQYPYGGYILNRPFTTSRRPMPVEGTAAYKELESNPEKAFRLTICS 780  
 Qy 781 ELQALVSIISIEILSKHASDEVYLGQRASIDWTSDKIALFAFEKFGKQLFEVENRIMERN 840  
 Db 781 ELQALVSIISIEILSKHASDEVYLGQRASIDWTSDKIALFAFEKFGKQLFEVENRIMERN 840  
 Qy 841 KEVNLKNSRSGPNLPYTLVPSNEGTLGRGIPNSISI 878  
 Db 841 KEVNLKNSRSGPNLPYTLVPSNEGTLGRGIPNSISI 878

RESULT 3  
 AAO27492  
 ID AAO27492 standard; protein; 880 AA.  
 AC AAO27492;  
 DT 06-NOV-2003 (first entry)  
 DE Balsam pear (Momordica charantia) lipoxigenase isozyme 2 protein.  
 KW Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;  
 KW fatty acid metabolite synthesis; signal molecule; growth regulation;  
 KW development regulation; plant development; wound response;  
 KW genetic mapping; hyperoxidation catalysis; Balsam pear; enzyme.  
 OS Momordica charantia.  
 XX US2003074593-A1.  
 PD 17-APR-2003.  
 XX 29-JAN-2002; 2002US-00059909.  
 PR 10-FEB-1999; 99US-0119597P.  
 PR 09-FEB-2000; 2000US-00501422.  
 XX (CAHO/) CAHOON E B.  
 PA (KINN/) KINNEY A J.  
 PA (KLEI/) KLEIN T M.  
 PA (LEET/) LEE J.  
 PA (PEAR/) PEARLSTEIN R W.  
 PA (RAFA/) RAFALSKI J A.  
 PA (SHEN/) SHEN J B.  
 PA (THOR/) THORPE C J.  
 PA (TING/) TINGEY S V.  
 PA (WENG/) WENG Z.  
 XX Caboon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;  
 PI Rafalski JA, Shen UB, Thorpe CJ, Tingey SV, Weng Z;  
 XX WPI; 2003-567325/53.  
 DR N-PSDB; AAL57712.

XX New isolated polynucleotides encoding plant lipoxigenases, useful in  
 PT genetic mapping, particularly in catalyzing hyperoxidation of  
 PT polyunsaturated fatty acids.  
 XX Claim 19; Page 23-25; 36pp; English.  
 XX This invention relates to novel nucleotide sequences which encode  
 CC proteins which have lipoxigenase activity. Lipoxigenases are membrane  
 CC bound ubiquitous enzymes which catalyze the hydroperoxidation of  
 CC polyunsaturated fatty acids in the first stage of fatty acid metabolite  
 CC synthesis. Products of this pathway are found as signal molecules  
 CC involved in growth and development regulation. A knowledge of the amino  
 CC acid sequence of lipoxigenases may allow the understanding of plant  
 CC development and wound response. The polynucleotides, polypeptides and  
 CC lipoxigenases of the invention may therefore be useful in genetic mapping  
 CC and particularly for catalyzing hydroperoxidation of polyunsaturated  
 CC fatty acids. The present sequence is the amino acid sequence of the  
 CC Balsam pear (Momordica charantia) lipoxigenase protein 2 of the invention  
 XX Sequence 880 AA;  
 SQ

Query Match 84.1%; Score 3933; DB 6; Length 880;  
 Best Local Similarity 81.7%; Pred. No. 0;  
 Matches 719; Conservative 83; Mismatches 76; Indels 2; Gaps 1;

Qy 1 MFGIGKNIIEGALNTTGDLAGSVINAGNILDVSSLGSKNKIKGVILMRSNVLDFTBFH 60  
 Db 1 MFGIGKSIIEGAVNTTGDLAGSVINAGNIVGRVNTIGGKTKGVVLMRSNVLDFTBFH 60  
 Qy 61 SNLDNFTLGGGVSFQLISATHTSNDSRGVGNKAYLERWLTSIFPLFAGESVFQINF 120  
 Db 61 SSLDGVTELLGGGISLQLISATHASNDSRGVKGAFLEWLTSVPLFAGESVFQVNF 120  
 Qy 121 QWDENFGFGAFPIKNGHTSEFFLKSLLDLDVPGYGRVHFDGNSVYSGRKKRIEPPA 180  
 Db 121 DWEENFGFGAFPIKNGHTSEFFLKSLLDLDVPGYGRVHFDGNSVYSGRKKRIEPPA 180  
 Qy 181 NHVYLPQSTPNPLRYREELNLRGDTGERKEWDRIYDYVYNDIADPDVGDH--RPI 238  
 Db 181 NHTCLPIDPDSLRKYREBELNLRGDTGERKEWDRIYDYVYNDLCDPNGGPNLVPI 240  
 Qy 239 LGGTEYPPRRGRTGRPRSRDHYESKLSPIMSLDIYVPKDNFGLKXSDFLGYTLK 298  
 Db 241 LGGSDQYPYRRGRTGRPPARKDHYESRLSDVMSLNIVYPRDENFGLKXADFLGTLK 300  
 Qy 299 ALSISIKPGLQSTEDVTNPFNPFNKEVDNLRERGPPIPNAPFKTLTDLTPPLKALVRN 358  
 Db 301 VLSTSIQPGESIFDSTPGCFKFEVDLPERGPIPLNIFKNUTEDLAPPLKAFURS 360  
 Qy 359 DGEKFLKPTPEVVKDNKIGWSTDEFAPEMLAGNPLLRLEAPPTSKLDPNVYGNQ 418  
 Db 361 DGERFLKYPTPOVTKDNKLGWRTDEFAREMIAGVNPLIIRLEVFPPSLKLDPHVYGNQ 420  
 Qy 419 NSTITFEHKKHGLDGLTVDEAMKQNLXYVDFHDLMPYLTRMNATSTKYATRILLK 478  
 Db 421 NSTMTTEEQIKHGLDGLTVDEAKENKLYILDHHDALMPYLRINISTKTATRILLFLK 480  
 Qy 479 DDGTLKPLVIELALPHPQGDQLGALSKLYFPAENGQVQKSIWOLAKAYTVNDVGYHQLIS 538  
 Db 481 DDSTLKPLAIELSLPHPQGDHEGALSKLYFPAENGVESAIWOLAKAYVAVNDSGYHQLNS 540  
 Qy 539 HMLHTHAVLEPPFVIATHRQLSVLHPHKLIVPHYKDTMETINASARQVLINANGLIETHY 598  
 Db 541 HMLHTHAVLEPPFVIATHRQLSVLHPHKLIVPHYKDTMETINASARQVLINAGLTESTQF 600  
 Qy 599 PSKYSMELSSILYKDWTFDQALPNNLMKRGGLAVEDSSAPHGRLRLINDYPFAVDGLDIW 658  
 Db 601 PAKYAMELSSYIKYKWKFPFDEALPTNLIKRGVAIEDSGSPHGVRLINDYPFAVDGLEIW 660  
 Qy 659 SAIKTVWQDYCCLYYKDDNAVQNDPHELOSWNLEKGHADKXHEPWPMPQOTLSELBS 718  
 Db 661 SAIKTVWTDYCSLYYKDDAIRNDVBLQSWWKEKLGHTDKDBPWPMPQOTLSELBS 720





XX PF 10-JUL-2000; 2000WO-EP006539.  
 XX PR 08-JUL-1999; 99DE-01031819.  
 XX PA (IPBP-) IPB INST PFLANZENBIOCHEMIE.  
 XX PI Feussner I, Hornung E, Rosahl S;  
 XX WPI; 2001-081054/09.  
 XX PT New nucleic acid encoding lipoxigenase useful for producing 11-  
 XX PT hydroperoxy- or hydroxy-arachidonic acid.  
 XX PS Disclosure; Fig 3; 18pp; German.  
 XX CC This invention describes a novel nucleic acid (I) encoding a potato  
 CC lipoxigenase protein, LOX, (II) is new. The invention also describes  
 CC (III), a sequence of 857 amino acids (aa), given in the specification; (2)  
 CC a vector (III) comprising (1); (3) a host cell (IV) comprising (1) or  
 CC (III); (4) a plant or part of a plant comprising (IV); (5) enhancing the  
 CC specificity of a plant lipoxigenase for position 11 of arachidonic acid;  
 CC comprising mutating at least one amino acid of the wild type lipoxigenase;  
 CC (6) producing 11-hydroperoxy-arachidonic acid or the reduced 11-hydroxy-  
 CC derivative comprises treating arachidonic acid with (II) and further  
 CC reducing the obtained hydroperoxy form to the hydroxy form; (7) the  
 CC arachidonic acid derivative, comprising a hydroperoxy group or a hydroxy  
 CC group at position 11. (II) is useful for producing 11- hydroperoxy-  
 CC and/or 11-hydroxy-arachidonic acid. The lipoxigenase is specific for  
 CC position 11 of arachidonic acid  
 XX SQ Sequence 857 AA;

Query Match 64.0%; Score 2992.5; DB 4; Length 857;  
 Best Local Similarity 64.9%; Pred. No. 1.5e-262;  
 Matches 552; Conservative 123; Mismatches 167; Indels 9; Gaps 4;

QY 37 LGGN---KIKGKVLMSNVLDTEFHNSLLDNFTLLGGVDFQLISATHT--SNDSR 90  
 DB 7 IGGHDSKKVGTVMKKKNAUFDFTLAGSLTDKIFALGQKVSFQLISSVQSPANGLQ 66  
 QY 91 GKVGKAYLERWLTISIPPLFAGESVFQINQWENFGFPFAGFFIKNGHTSEFFLKSLTLD 150  
 DB 67 GKHSNPAYLENFLTTLAAGETAFGTFDWNEBFGVPGAFIKNTHINEFFLKSLTLE 126  
 QY 151 DVPQGYGRVHFCNWSVYPSGKDKRIEFANHVLPSTQNPPLKRYEELWNLRGDGTG 210  
 DB 127 DVFNHGKVFVCSNWSVYPSFRYSKDRIFFAQNPYLPSETPELLKRYENELLTURGDTG 186  
 QY 211 ERKEWDRIYDVYNDIADPDVGDH--RPILGGTTEYPPRRGRTPRRSRDHNYESRL 268  
 DB 187 KREAMDRIYDVYNDLGNPDQGEQNVRTLLGGSADYPPRRGRTPRTDTPKSESRI 246  
 QY 269 SPMSLDIYVPKDNFGLKMSDFLGYTLKALTSIKPQLOSIFDVTNPEDNFKVDNL 328  
 DB 247 PULISLDIYVPRDERFGLKMSDFLTALKSIQVIFLPELHALFDGTPNEPDSFEDVRL 306  
 QY 329 FERGFPIPFN-AFKTLTLEDTPPLFKALVRNDGKFLKFTPPVVKDKNGKWSDEEFAR 387  
 DB 307 YEGGIKLQGGPLFKALTAAPLEMMKELLRTDGEGLRFPFTPLVKSKTAWRTDEEFAR 366  
 QY 388 EMLAGNELLIRLEAPPTSKLDNPNVGNQNSITTEBHIKHGLDGLTVDAMKQNLXI 447  
 DB 367 EMLAGNPIIISRLQEFPPKSKLDPEAYGNQNSITTAEBHIEDKLDGLTVDAMNNKLF 426  
 QY 448 VDFHALMPYLRMTATSKYVATVTLKLLKDDGTLKPLVLTELALPHPOGDLGAISKLY 507  
 DB 427 LNHHDVLPYLRINRTTKYVASTLLFLQDNGSLKPLALELSLPHPDGQDFVISKVY 486  
 QY 508 FPAENGQKSIWQAKAYVTVNDVGVHQLISHWLTHTAVLEPFFVIATHRQLSLVHPHKL 567  
 DB 487 TPDQGVSESSIWQAKAYVAVVNDVGVHQLISHWLTHTAVIEPFFVIATHRQLSLVHPHKL 546

QY 568 LVPHYKDTMFINASARQVLINANGLIETHYPSKYSMELSSILYKDWTFPDQALPNNLMK 627  
 DB 547 LYPHFEDTWNINAMARQVLINANGVLESTVFPFKFAMEMSAVVYKDWTFPDQALPADLVK 606  
 QY 628 RGLAVEDSSAPHLRLINDYFPAVDGLDINSAIKTWQDYCCLYKDDNAVONDFELQS 687  
 DB 607 RGVAVEDSSSPGVRLLIEDYFPAVDGLEINSAIKSWTDYCSFYGSDEELKDKNELQA 666  
 QY 688 WYNELREKGHADKKEPMPKQTLSELIESCTTIWIASALHAANFQGPYGGYILNR 747  
 DB 667 WKELREVGCHGDKNEPMPMETQELIDSTTIWIASALHAANFQGPYAGYLPNR 726  
 QY 748 PTTSRFMPVEGTABYKELESNPKAFIETICSELOALVSIISIIILSKHASDEVYLQOR 807  
 DB 727 PTVSRFMPPEPGTPPEYELKKNPKAFKLTITTAQLQTLGLVSLIELSRHTTDEIYLQOR 786  
 QY 808 ASIDWTSKIALAEAFKFGKNLFEVENRIMENKVNKLKRSQPNVLPVTLVPSSEGL 867  
 DB 787 ESEFWTKDEPLAARDKFGKLTIDIEKLIQRNGNLTNRSGPVNAPYTLFFPISSEGL 846  
 QY 868 TCRGIPNSISI 878  
 DB 847 TCRGIPNSVSI 857

RESULT 7  
 ABP70404  
 ID ABP70404 standard; protein; 862 AA.  
 XX AC ABP70404;  
 XX DT 07-APR-2003 (first entry)  
 XX DE Amino acid sequence of tobacco lipoxigenase-1 (LOX-1).  
 XX KW Lipoxigenase-1; LOX-1; enzyme; plant; dioxygenation;  
 KW polynaturated fatty acid; pentadiene; disease resistance; Solanacea;  
 KW tobacco; tomato; potato; pepper.  
 OS Nicotiana tabacum.  
 XX FN W0200299112-A2.  
 XX PD 12-DEC-2002.  
 XX PF 06-JUN-2002; 2002WO-FR001943.  
 XX PR 07-JUN-2001; 2001PR-00007470.  
 PR 07-NOV-2001; 2001PR-00014358.  
 XX PA (RHOB-) RHOBIO.  
 XX PI Mene-Saffrane L, Esquerre-Tugaye M, Fournier J, Beffa R;  
 PI Grosjean-Cournoyer M;  
 XX DR WPI; 2003-156858/15.  
 DR N-PSDB; ABZ68210.  
 XX Reducing sensitivity of plants to diseases and pathogens, by  
 PT overexpressing a lipoxigenase, also vectors and cassettes for the process  
 PT and transformed plants.  
 XX Claim 7; Page 39-41; 47pp; French.  
 CC The present sequence represents a lipoxigenase-1 (LOX-1) gene. LOX-1 is  
 CC an enzyme that catalyses the dioxygenation of polyunsaturated fatty acids  
 CC having a pentadiene system. Overexpression of LOX-1 can be used to reduce  
 CC the sensitivity of plants to diseases and attack by pathogens.  
 CC Overexpression of LOX-1 improves resistance to viruses, bacteria, fungi  
 CC and insects, in a wide range of crops, particularly the Solanaceae, e.g.  
 CC tobacco, tomato, potato and pepper  
 XX Sequence 862 AA;





QY 195 KYREELNLRGCGTGERKWDRIYDYVDYNDIADDPVGDH--RPILGGTTEYPYRGR 252  
 Db 178 KYREELNLRGCGTGERKWDRIYDYVDYNDIADDPVGDH--RPILGGTTEYPYRGR 237  
 QY 253 TGRPRSRDHYESELSPMSLDIYVVDXENFGHLKMSDFLGYLTKALISIKPGLQSI 312  
 Db 238 TGRKTRKDPNSES-----SNDVYLPDRDEAFGLKSSDFLTGKLSQVSNVPLLSQAF 292  
 QY 313 DV--TPNEFDNFKVDNLFERGFPPFNKFTLTDLTLP-PLFKALVRNDGEKLEKPTP 369  
 Db 293 DNFTEPRFDSDEVHGLYSOGIKLPTD---IISKISPLEVLKEIFRTDGEQALKPFP 348  
 QY 370 EYVKNKICWSDEEFAREMLAGNPLIRLEAFPPPTSKLDPNVYQNSNTIIEEIKH 429  
 Db 349 KVIQVSKSAWMTDEEFAREMLAGNPNLIRCLKOPPPSKLDSQVYGDHTSQITKEHLEP 408  
 QY 430 GLDGLTVDEAMKQNLRIYVDHDLMPYLTRMNTATSTYATRLILLKDDGTUKPLVIE 489  
 Db 409 NLEGLTVDEAIQNKELFLDHDPIYPLIRINATSTKAYATRLIFLKNDDGTURPLAIE 468  
 QY 490 LALPHQDQDLGALISKLYFPAENGCKSIWOLAKAYTVNDVGVHOLISHLHVALEP 549  
 Db 469 LSLPHQDQDQSAFQFPLPADEGVESIWLLAKAYVVDNSCHQLVSHWLNTHAVPEP 528  
 QY 550 FVIATHROLSVLHP IHKLLVPHYKDTMFINASARQVLINANGLIETHYPSKYSMELSSI 609  
 Db 529 FFIATNRHLSVVHPYIKLLHBYRTMNINGLARLSLVNDGCVIEQTFPLWGRYSVMSAV 588  
 QY 610 LYKDWTFDQALPNLMKRGAVESAPHGRLLLINDYPAVDGLDIWSAIKTWODYC 669  
 Db 589 VYKDWTFDQALPNLMKRGAVESAPHGRLLLINDYPAVDGLDIWSAIKTWODYC 648  
 QY 670 CLYKDDNAVQDFELQSWNELREKGHADKHEFWPMPKQMTSELIESCTTIWIASAL 729  
 Db 649 FLYKSDDTLREDPELQACWELVEVGHGDKKNEFWPMPKQMTSELIESCTTIWIASAL 708  
 QY 730 HAAVNFQYPIGGYILNRPTRSRMPPEVGTAEYKELESNEKAFRLTICSELQALVIS 789  
 Db 709 HAAVNFQYPIGGYILNRPTRSRMPPEVGTAEYKELESNEKAFRLTICSELQALVIS 768  
 QY 790 ITEILSKHASDRVYLQORASIDWTSKIALFAFKFGKXNLFVEVNERIMERKEYNLKURS 849  
 Db 769 VIEILSRHASDEVYIGERDNPWTSIDTRALEAFKFGKXNLFVEVNERIMERKEYNLKURS 828  
 QY 850 GPVNLPTLLVPSSNEGHTGRGIPNSISI 878  
 Db 829 GPVQMPYTLLLPSSXEGHTFRGIPNSISI 857

RESULT 9  
 ID ABG30569 standard; protein; 865 AA.  
 AC ABG30569;  
 XX  
 XX  
 DT 07-OCT-2002 (first entry)  
 DE Glycine max low-lipoxygenase 2 (LOX-2).  
 XX  
 XX Lipoxygenase-1; LOX-1; beverage; malt; beer; organoleptic property;  
 KW brewing; trans-2-nonenal; flavour stability; storage; shelf-life;  
 KW low-lipoxygenase 2.  
 XX  
 XX Glycine max.  
 OS  
 XX WO200253721-A1.  
 PN  
 XX  
 PD 11-JUL-2002.  
 XX  
 XX 22-JAN-2001; 2001WO-IB000207.  
 XX  
 XX 29-DEC-2000; 2000US-00751687.  
 PR 29-DEC-2000; 2000WO-IB002045.

XX (CARL-) CARLSBERG RES LAB.  
 PA (HETB-) HEINEKEN TECH SERVICES BV.  
 PA (BRAS-) BRASSERIES KRONENBOURG SA.  
 XX  
 PI Duma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;  
 PI Schmitt N, Heister JC, Van Mechelen JR;  
 XX WPI; 2002-557742/59.  
 DR Novel barley plants having low lipoxygenase activity useful in the  
 XX production of plant products such as malt or brewed beverages,  
 PT particularly beer having increased stability and flavor.  
 PT  
 XX Disclosure; Fig 22A-B; 112pp; English.  
 PS  
 XX The invention describes a barley plant (I) having a mutant lipoxygenase-1  
 CC (LOX-1) protein, the plant or plant portion characterised by a reduction  
 CC or absence of LOX activity as compared to a non-mutated control, or  
 CC comprising a heterologous nucleic acid sequence expressing an antisense  
 CC sequence to a transcribed region of barley lox-1 gene, operably linked to  
 CC a promoter and a transcription terminator sequence. (I), a plant (II)  
 CC produced using (I) or a plant product (III) is useful in the manufacture  
 CC of a beverage, preferably malt or beer, for stabilising organoleptic  
 CC properties of a brewed product over a measured period of time as compared  
 CC to a control brewed product produced using a non-mutated barley plant or  
 CC its portion, grain or plant progeny, or plant product, and for the  
 CC manufacture of a brewed product having reduced levels of free trans-2-  
 CC nonenal over a measured period of time or under conditions of elevated  
 CC storage temperature, as compared to a control brewed product produced  
 CC using a non-mutated barley plant or its portion, grain or plant product.  
 CC Beer with significantly enhanced flavour stability, both during storage  
 CC and on exposure to elevated storage temperatures is obtained. These  
 CC properties enhance the quality of beer and are useful to extend its shelf  
 CC -life and reduce the need to cool beer during transport and storage. This  
 CC is the amino acid sequence of the Glycine max low-lipoxygenase 2 (lox-2)  
 CC protein  
 XX  
 SQ Sequence 865 AA;  
 Query Match 57.5%; Score 2690; DB 5; Length 865;  
 Best Local Similarity 58.4%; Pred. No. 5.4e-235;  
 Matches 513; Conservative 127; Mismatches 194; Indels 44; Gaps 8;

QY 23 VINAGNILDVSSLSGGNKIKGKVMILMSNVLDTFEFH-----SNLL 64  
 Db 10 ILNRG-----GGHKIGTVVLMRKQVLDNFNSVADLTGKNGVGLIGTLNVLVSTL 59  
 QY 65 DNFTLLGGVSFQLISATHTSNDRGKVGKNKAYLERWLTGIPPLFAGESVFCINFWDE 124  
 Db 60 DNLTAFLGESVALQLISATKPLANGKGVKQDTFLEGIIVSLPTLGAGESAFNIQFWE 119  
 QY 125 NFGFCAPPIKNGHTSEFFLSKSLTLDVPGVGRVHFDNCNWSVPSGRYKRIIPANHY 184  
 Db 120 SMGIFGAFIKNYMQVEFYLSLTLEDVFNQGTIFVCSNWSYNTKLYKSVRIIPANHY 179  
 QY 185 LPSQTNPLRKYREBELNLRGDTGGERKWDRIYDYVDYNDIADDPVGDH--RPILGGT 242  
 Db 180 VSETFPAALVGYREBELNLRGDTGGERKWDRIYDYVDYNDIADDPVGDH--RPILGGT 239  
 QY 243 TYPYPRRGTRQPRSRDHYESELSPMSLDIYVVDXENFGHLKMSDFLGYLTKALIS 302  
 Db 240 STHPYPRRGTRQPRSRDHYESELSPMSLDIYVVDXENFGHLKMSDFLGYLTKALIS 293  
 QY 303 SIKPGLQSIQFV--TPNEFDNFKVDNLFERGFPPFNKFTLTDLTLPFKALVRNDG 360  
 Db 294 YVLPAFESVDFLNFTEPRFDSDEVHGLYSOGIKLPTD---IISKISPLEVLKEIFRTD 350  
 QY 361 EKFLFPPTPEVVKNDKIKGWSDEEFAREMLAGNPLIRLEAFPPPTSKLDPNVYQNS 420  
 Db 351 EQVLKFPFPHVIVQSKSAWMTDEEFAREMLAGNPNLIRCLKOPPPSKLDSQVYGDHTSQ 410  
 QY 421 TITEEHKIGLGLTVDEAMKQNLRIYVDHDLMPYLTRMNTATSTYATRLILLKDDGT 480

Db 411 KITADAL-DLDGTVDEALASRELFWLDVHDVPMPIRRINQYAKAYATRIPLFREN 468  
Qy 481 GTLAKPLVIELALPHPOGDLGALSKLYPAENGQKSIWOLAKAYVTVNDVGHOLISHW 540  
Db 469 GTLKPVAIEUSLPHPGAGLSGAVSQVILPAKEGVESTIWLLAKAYVVNDSCYHQLMSHW 528  
Qy 541 LHTHAVLEPFFVIATHROLSVLHPHKLIVPHYKDTMFINASAROVLINANGLIETTHYPS 600  
Db 529 LNTHAVLEPFFIATNRHLSALHPHYKLLTPHYRDTMNAIARQSLINADGIEKSLPS 598  
Qy 601 KYSMELSSILYKDWTFDQALPNLMKRGGLAVEDSSAPHGLRLILLINDYPFAVDGLDIWSA 660  
Db 589 KHSVEMSAVYKXNVFTDQALPADLIKRGVAIKDPSAPHGLRLILLIEDYPYAVDGLLEIWA 648  
Qy 661 IKTWQDYCCLYKDDNAVONDFELQSWNELREKKGHADKHEBPWKMTLSLIESCT 720  
Db 649 IKTWQEVVSLYIARDDDVDKDESELOQWKEAVEKGHGLDKXKFWPKLOTIELVEICT 708  
Qy 721 TIWIASALHAANFGQYGYILNRPRTTSRRPMPVGTABYKELSENPEKAPLRITCS 780  
Db 709 IIIWTASALHAANFGQYGYILNRPRTTSRRLLPEKGTPEYEMVKSHQKAYLRITIS 768  
Qy 781 ELQALVSTIIEILSKHASDEVYLGORASIDWTSKIALEAFKFKGNLFEVENRIMERN 840  
Db 769 KQTLVDLVSVIEIISRHASDEVYIGORDNPHTSDSKALQAFQKGNLKEIEKJARKN 828  
Qy 841 KEVNLKNSRGPVNIPTYLLVPSSNEGLTGRGIPNSISI 878  
Db 829 NDQSLNRLGVPQLPYTLIHNS-EGLTGCRGIPNSISI 865

## RESULT 10

AAR24042  
ID AAR24042 standard; protein; 864 AA.

XX AC AAR24042;

XX DT 08-DEC-1992 (first entry)

XX DE Lipoxigenase.

XX KW Soybean; transformation; disease resistant; pest resistant.

XX OS Glycine max.

XX XX JP04144687-A.

XX PD 19-MAY-1992.

XX PF 05-OCT-1990; 90JP-00266687.

XX PR 05-OCT-1990; 90JP-00266687.

XX PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

XX WPI; 1992-214124/26.

XX DR N-PSDB; AAQ25591.

XX PT Structural gene of soybean lipoxigenase - enables mass prodn. of the lipoxigenase and creates plants with high resistance to disease and pests.

XX PS Disclosure; Fig 1; 7pp; Japanese.

XX CC The sequence given is soybean lipoxigenase. This protein is expressed in the sprouting time of soy bean. The DNA encoding this sequence can be ligated into a plasmid and this plasmid used to transform E. coli. Using this transformant, mass production of lipoxigenase is possible. It can also be used to create a plant highly resistant against disease and pest

XX SQ Sequence 864 AA;

Query Match 56.5%; Score 2639.5; DB 2; Length 864;  
Best Local Similarity 58.0%; Pred. No. 2.1e-230;  
Matches 503; Conservative 125; Mismatches 202; Indels 37; Gaps 7;  
Qy 39 GNKIKGKVLKMSNVLDFTFHS-----NLDNFTELLGGGV 76  
Db 8 GOKIKGTVMKPNVLDNFNAITSIGKGVVIDTATGILGGVSLVGGVDTATSFILGRNIS 67  
Qy 77 FOLISATHTSNDRGKGVNKAYLERWLTSIPLPAGESVFOINFDOWNFPPGGAFFIKN 136  
Db 68 MQLISATQDGGSGKGVKEVLEKHLPTLPLGARQDAFSIFFEWDASFGIPGAFYIKN 127  
Qy 137 GHTSEFFLKSLLDVPVGYRVHPCNSWVPSGYKKDRIPFANHHVLPSPQTPNPKRY 196  
Db 128 FMTDSFFLVSVKLEIDPNHGTIEFVCSWVNFYSKKNRIPFVNDTLPSPATPLNLY 187  
Qy 197 REEELNWLKGGTGERKEWDRIYDVNDIADPDVGDHRPILGCTTETVYVPRRGTGRP 256  
Db 188 RKEEELVULKGGTGRKODFRIYDVNDLGNPGGDPRIPLGSSSYPIPRRVRTGRE 247  
Qy 257 RSRDRHNTESRLSPIMSLDIYVPKDNFEGHLMKMSDFLGYTLKALSIKPGIQS-IFD-- 313  
Db 248 RRTDTPNSEK-----PGEVYVPRDENFGLKSSDFLYGKMSLSDHVIPLPKSAIFQLR 301  
Qy 314 VTPNEDNPKVDNLPFERGFPIPPNAFKTLTDLTP-PLFKALVNDGKELKPTPEV 372  
Db 302 VTSSEFSEFEDVRSYEGGIKLPTD----ILSQISPLPALKEIFRTDGENVLQFPFPHVA 357  
Qy 373 KDNKIGWSTDEEFAREMLAGNPILLIRLEAPPTSKLDPNVYQNSQNTIEEHKKGGLD 432  
Db 358 KVSXSGWMTDEEFAREVIAGVNPVIRRLQEPFPPKSTLDPTLYGDTSTIIEKELEINNG 417  
Qy 433 GLTVDEAMKQNLVYVDFHDLMPYLTMRNATST-KYATRTLLLLKDDGLTKPLVIELA 491  
Db 418 GVTVEEALSTQRLFDYQDAFIPYLTRINSIPLTAKAYATRIPLFKDDGLTKPLAIELS 477  
Qy 492 LPHPOGDOLGALSCLYFPAENGQKSIWOLAKAYTVNDVGYHOLISHMLTHAVLEP 551  
Db 478 KHPDGDNLGPESIVVLPAEGVDSTIWLAKAHVINDSGYHQLVSHWLNTHAVNEPFA 537  
Qy 552 IATHRQLSVLPHIKLLVPHYKDTMFINASAROVLINANGLIETTHYPSKYSMELSSILY 611  
Db 538 IATNRHLSVLHPHYKLLVPHYRDTNINGLARQSLINADGIEKSFPGKYSIEMSSVY 597  
Qy 612 KDWTPDQALPNLMKRGGLAVEDSSAPHGLRLILLINDYPFAVDGLDIWSAIKTWQDYCCL 671  
Db 598 KMWVFTDQALPADLVKRGGLAIEDPSAPHGLRLVIEDYPYAVDGLBEIWDKATWVHEYVSL 657  
Qy 672 YIKDDNAVQDFELQSWNELREKKGHADKHEBPWKMTLSSELIESCTTIWIASALHA 731  
Db 658 YIPTDAAVQDDTELQAWKKEAVEKGHGLKKEKPMWPKMTTEDLIQSCSIIVWTASALHA 717  
Qy 732 AVNFGQYGYGVLINRPRTTSRRPMPVGTABYKELSENPEKAFRTICSELOALVSIIL 791  
Db 718 AVNFGQYGYGVLINRPRTTSRRPMPVGTABYKELSENPEKAFRTICSELOALVSIIL 777  
Qy 792 EILSKHASDEVYLGORASIDWTSKIALEAFKFKGNLFEVENRIMERNKEVNLKNSRGP 851  
Db 778 EILSKHASDEVYLGORASIDWTSKIALEAFKFKGNLFEVENRIMERNKEVNLKNSRGP 837  
Qy 852 VNLPTVLLVPSSNEGLTGRGIPNSISI 878  
Db 838 VOLPYTLHRSSEGLTFKGIPIINSISI 864

## RESULT 11

AAR50220  
ID AAR50220 standard; protein; 853 AA.

XX AC AAR50220;

XX DT 08-NOV-1994 (first entry)

DE Soybean lipoxigenase L-4.  
 KW Soya; Soybean; lipoxigenase L-4; transgenic plant.  
 XX Glycine max.  
 OS  
 XX JP06062864-A.  
 PN 08-MAR-1994.  
 XX  
 XX 18-AUG-1992; 92JP-00219480.  
 XX 18-AUG-1992; 92JP-00219480.  
 XX (MITS-) MITSUI GYCSAI SHOKUBUTSU BIO KENKYUSHO.  
 XX WPI; 1994-121126/15.  
 DR N-PSDB; AAQ44750.  
 XX  
 XX Soybean lipoxigenase L-4 gene - used in the production of transgenic plants.  
 PT  
 PT  
 XX Disclosure; Page 6-11; 13pp; Japanese.  
 PS  
 XX The soybean lipoxigenase L-4 gene was isolated from a known soybean genomic DNA clone. The gene is expressed at high levels in the cotyledon, hypocotyl, roots and first leaf. The coding region is made up from 9 CC exons and codes for a protein having 853 amino acids  
 CC  
 XX Sequence 853 AA;  
 SQ  
 Query Match 55.4%; Score 2591; DB 2; Length 853;  
 Best Local Similarity 57.4%; Pred. No. 5.4e-226;  
 Matches 492; Conservative 133; Mismatches 204; Indels 28; Gaps 10;  
 QY 39 GNKIKGVILARSNVLDPTFPHS--NLIDNFTELLGGV-----SFQIISATHTS 86  
 DB 8 GQKIKGTVMVQKNVLDINSITSVGGIVDQGLGFGISAVDALTPAATKISQILISAT-KA 66  
 QY 87 NDSRGKGNKAYLERWLTISPLPAGESVFQINQWENDFGPGAFPIKNGHSEPLKS 146  
 DB 67 DGGKGIKGTNLKGI-T-LPTLAGEQAYDNFEDWDFGPGAFYIKNFQMEFYLS 125  
 QY 147 LTLDVPGYGVHFDGNSWVYPSGRYKDKRIFFANHYVLPSTPNPLRYKREELWNLRG 206  
 DB 126 LILEDIPNHGTHFVCSWVYNSKNYKTDRIFFANNYLPSETPAPLLKYREELKNVVG 185  
 QY 207 DGTGERKWDRIYDVYVNDIADPDVGMH--RPILGTTTEYPYPRRGTRGRPRRDHNY 264  
 DB 186 DGTGERKWDRIYDVYVNDLGNPDSDGKYARPVLGSA-LPYPRRBRTRGRGTRKDPNS 244  
 QY 265 ESRLSPIMSLDIYVPCDNFGLKMSDFGLTKALSIKPGLSQIFD--VTPNEPDFNF 322  
 DB 245 EK-----PSDFVYLPDRBAFHLKSSDFLAYCIKSVSQDVLPLVTDAPDGNLSLEPDFNF 299  
 QY 323 KEVDNLFERGFPIPFNAFKTLTDLTPPLFKALVRNDGERKPLKPTPEVVKDNKNGWSTD 382  
 DB 300 AEVHKLYEGGVTLPTN--FLSKIAPIPVKEIFRTDGEQPKYPPPKVMQVDSAMMTD 356  
 QY 383 BEFARMLAGNPLLIRLEAFPTSKLDPNVQNSSTTEHIIKHGLDGLTVDEAMKQ 442  
 DB 357 BEFARTTAGLNPNVPIKIEFFUSSKLDQYAGDHTCIITAKEHLEPNLGLTVQAIQN 416  
 QY 443 NRLYIVDFHDMPLTETMNTATSTKYATRTLLKDDGTLKPLAVIELALPHFGQDLGA 502  
 DB 417 KKLFLDHRDYLIPYLRKINANTKTATRTIFELKDDGTLTPLAIELSKPHFQGEYGP 476  
 QY 503 ISKLYFPBENGQKSIWOLAKAYTVNDVGHQIISHWLTHAVLEFPVIAHQRLSVLH 562  
 DB 477 VSEVTVPASEGVEAYIMLLAKAYVVDNDACYHQIISHWLSHTAIVEFPVIAHQRLSVH 536  
 QY 563 PIHKLVLPHYKDTWPFINASARQVLINAGLTETHTHPSKYSMELSSLYLDWTFPPQALP 622

DB 537 PIYKLLFPHYDTMNSLARKALVNADGIIETKFLWGRYSMEMSAVIYKDWVFTDQALP 596  
 QY 623 NNLKRGGLAVEDSSAPHGLRLINDYPEAVDGLDITWSAIKTVQDYCCLYYKDDNAVQND 682  
 DB 597 NDLVTRGVAVKDPSPAPHGVRLLIEDYPVASGLEIWDKISWQVYFVYKSEDEELQD 656  
 QY 683 FELQSWNELREKGHADKKHPEWPKMQTSLSELIESCTTIWIWASALHAANFGQYPYGG 742  
 DB 657 PELQAWKVELVEVGHGDLKDEWQKQVOTRELVESAILIWIWASALHAANFGQYPYGG 716  
 QY 743 YILNRPPTTSRRFMPVEVGTAEYKELESNPEKAFIRTCSELQALVSIISIIELSKHASDEV 802  
 DB 717 LILNRPPTTSRRFMPPEKSGPEYDALAKNPEKFKITITGKKTDLITLTVIELSRHASDEF 776  
 QY 803 YLQQRASID-WTSDKIALEAFKFGKNIFFVENRIMERNKEVNLKNSGPNLPYTLVLP 861  
 DB 777 YLGQRDGGDYWTS DAGPLEAFKRFKGLKEIEKKLIEKNKDETLNRYGPAKMPYTLVLP 836  
 QY 862 SSNEGLTGRGIPNSISI 878  
 DB 837 SSEGLTFRGIPNSISI 853  
 RESULT 12  
 ABG30568  
 ID ABG30568 standard; protein; 839 AA.  
 XX AC ABG30568;  
 XX DT 07-OCT-2002 (first entry)  
 XX Glycine max low-lipoxygenase 1 (LOX-1).  
 XX Lipoxygenase-1; LOX-1; beverage; malt; beer; organoleptic property;  
 XX brewing; trans-2-nonenal; flavour stability; storage; shelf-life;  
 XX low-lipoxygenase 1.  
 XX Glycine max.  
 XX WO200253721-A1.  
 XX 11-JUL-2002.  
 XX 22-JAN-2001; 2001WO-IB0002007.  
 XX 29-DEC-2000; 2000US-00751687.  
 XX 29-DEC-2000; 2000WO-IB002045.  
 XX (CARL-) CARLSBERG RES LAB.  
 XX (HETB-) HEINEKEN TECH SERVICES BV.  
 XX (BRAS-) BRASSERIES KRONENBOURG SA.  
 XX Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;  
 XX Schmitt N, Heistek JC, Van Mechelen JR;  
 XX WPI; 2002-557742/59.  
 XX Novel barley plants having low lipoxygenase activity useful in the  
 XX production of plant products such as malt or brewed beverages,  
 XX particularly beer having increased stability and flavor.  
 XX Disclosure; Fig 22A-B; 112pp; English.  
 XX The invention describes a barley plant (I) having a mutant lipoxygenase-1  
 XX (LOX-1) protein, the plant or plant portion characterised by a reduction  
 XX or absence of LOX activity as compared to a non-mutated control, or  
 XX comprising a heterologous nucleic acid sequence expressing an antisense  
 XX sequence to a transcribed region of barley lpx-1 gene, operably linked to  
 XX a promoter and a transcription terminator sequence. (i), a plant (ii)  
 XX produced using (i) or a plant product (iii) is useful in the manufacture  
 XX of a beverage, preferably malt or beer, for stabilising organoleptic  
 XX properties of a brewed product over a measured period of time as compared  
 XX to a control brewed product produced using a non-mutated barley plant or







**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2004, 11:56:59 ; Search time 49.1316 Seconds  
(without alignments)  
922.575 Million cell updates/sec

Title: US-09-937-908-1  
Perfect score: 4675  
Sequence: 1 MFGIGKNIIEGALNTTGDLA.....LVPSSNEGLTGRIKPSIS1 878

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/6C\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2791	59.7	857	4	US-09-751-687-17
2	2690	57.5	865	4	US-09-751-687-16
3	2582.5	55.2	839	4	US-09-751-687-15
4	2522.5	54.0	864	4	US-08-810-268-3
5	2438	52.1	862	4	US-09-751-687-9
6	2431	52.0	862	4	US-09-751-687-12
7	2424	51.9	864	4	US-09-751-687-18
8	495.5	10.6	677	3	US-09-061-768A-4
9	495.5	10.6	677	4	US-09-764-246-4
10	484	10.4	711	4	US-09-547-435-2
11	484	10.4	867	4	US-09-547-435-24
12	479	10.2	556	4	US-09-547-435-6
13	473	10.1	576	3	US-09-061-768A-2
14	473	10.1	676	4	US-09-764-246-2
15	466	10.0	692	4	US-09-252-991A-19668
16	457.5	9.8	701	3	US-09-087-727-2
17	457.5	9.8	701	4	US-09-853-053-2
18	427.5	9.1	662	3	US-09-061-768A-25
19	427.5	9.1	662	4	US-09-764-246-25
20	426.5	9.1	663	4	US-09-641-638-653
21	416.5	8.9	582	3	US-09-413-814-83
22	409.5	8.8	615	4	US-09-547-435-10
23	409.5	8.8	771	4	US-09-547-435-28
24	404.5	8.7	460	4	US-09-547-435-12
25	359	7.7	291	4	US-09-547-435-14
26	284.5	6.1	195	4	US-09-547-435-20
27	238	5.1	489	4	US-09-547-435-4

28	238	5.1	645	4	US-09-547-435-26	Sequence 26, Appl
29	233	5.0	334	4	US-09-547-435-8	Sequence 8, Appl
30	137	2.9	925	4	US-09-924-097A-14	Sequence 14, Appl
31	135.5	2.9	1541	3	US-08-296-791-3	Sequence 3, Appl
32	135.5	2.9	1541	4	US-09-839-996-3	Sequence 3, Appl
33	135.5	2.9	1541	4	US-10-080-505-3	Sequence 3, Appl
34	135.5	2.9	1541	5	PCT-US95-10661A-3	Sequence 3, Appl
35	134.5	2.9	139	4	US-09-547-435-18	Sequence 18, Appl
36	126.5	2.7	990	2	US-08-392-625-20	Sequence 20, Appl
37	126.5	2.7	990	2	US-08-466-961A-20	Sequence 20, Appl
38	120	2.6	990	2	US-08-645-193B-15	Sequence 15, Appl
39	113.5	2.4	945	4	US-09-198-452A-1030	Sequence 1030, Ap
40	113	2.4	69	4	US-09-547-435-16	Sequence 16, Appl
41	110.5	2.4	720	2	US-08-840-238-1	Sequence 1, Appl
42	110.5	2.4	720	2	US-08-505-448A-1	Sequence 1, Appl
43	110	2.4	514	4	US-09-540-236-2267	Sequence 2267, Ap
44	109.5	2.3	1545	3	US-08-296-791-4	Sequence 4, Appl
45	109.5	2.3	1545	4	US-09-839-996-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-751-687-17  
; Sequence 17, Application US/09751687  
; Patent No. 6660915  
; GENERAL INFORMATION:  
; APPLICANT: Douma, Anneke  
; APPLICANT: Doderer, Albert  
; APPLICANT: Cameron-Mills, Verena  
; APPLICANT: Skadhauge, Birgitte  
; APPLICANT: Rech, Lene  
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY  
; FILE REFERENCE: 11225.11US01  
; CURRENT APPLICATION NUMBER: US/09/751,687  
; CURRENT FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 857  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-751-687-17

Query Match	59.7%;	Score 2791;	DB 4;	Length 857;
Best Local Similarity	60.3%;	Pred. No. 9.3e-267;		
Matches 524;	Conservative 131;	Mismatches 182;	Indels 32;	Gaps 7;
Qy	28	GNILDRVSSLGNGKNGKVMRSNVLDFTPEHS	-----NLLDNFTLLGGG	74
Db	3	GGLLHR-----GHKINGTVLMRKNVLDVNSVTSGGIQGLDLVGLTDLTITAFGLRS	57	
Qy	75	VSPQLISATHSNDGRGKVGKXAYLERWLTSIPPLFAGESVFQINFQMDENFGFGAPPI	134	
Db	58	VSLQLISATKADANGKGLKATFLEIGITSITLTCAGQSAFKINFDWDDGSGIFQAFVI	117	
Qy	135	KNGHTSEFFKLTLDDVEGYGRVHFDCNSWYPSGRYKRRIFFFANHYVLESQTPNPLR	194	
Db	118	KNFQTEFFLVSLTLEDIENHGSIHFCVNSWYNAKLPKSDRIFFANQTYLPSETPAPLV	177	
Qy	195	KYREELNLRGDGGGERKEMDRIVDYVNDIADPDYGDH--RPLGGTTEYPPYRGR	252	
Db	178	KYREELNLRGDGGGERKEMDRIVDYVNDIADPDYGDH--RPLGGTTEYPPYRGR	237	
Qy	253	TGRPSRRDHNYESRLSPIMSLDIYVKDENFNGHLMKMSDFLGYTLKALISIKPGIQTIF	312	
Db	238	TGRKPTRKDPNSES-----SNDVYLPRDEAFGLKSSDFLYGLKSVQNVLLQLQSAF	292	
Qy	313	DV--ITNEFDNKVDNLFERFPPFPNAFKTLTDLTLP-PLFKALVRNDGKFLKFPPTP	369	
Db	293	DLNFTPREFDSFDEHGLYSGGIGKLPD-----IISKISPLPVKIFRDTGDEALKKPPPP	348	







Db 295 DSFQDIINLYEGGKLPKVAALBRLKQFPLQIIDLPLPVGGDILLKLPVPHIIOENKQA 354  
Qy 379 WSTDEEFAREMAGNPLIRLEAFPPSKLDENVYGNONSTITEEHIKHGLDGLTVDE 438  
Db 355 WRTDEEFAREVLAVNPNWIRLTFEPKPSLDSKSGDHTSTITASHIEKNLEGLTVQ 414  
Qy 439 AMQNRLVYVDFHDMALPYLFRM-NATSTKTYATRTLLKDDGTLKPLVIELALPHPOG 497  
Db 415 ALESNRLVILDHDRFMEFLDVNNLPGNFTYATRTLLFLRGDGRLTPLAIELSEPIIQ 474  
Qy 498 DQLAGISKLYPAENG-VOKSIWOLAKAYVTVNDVGVHOLISHWLHVALEPPIATHR 556  
Db 475 GLTTAKSKYVTVPSGSGVEGWELAKAYVAVNDGWHQLVSHHNLTHAVNEPPIVSTNR 534  
Qy 557 QLSVLHPIHKLVLPHYKDTMFINASARQVLINANGLIETTHYPYSKYSMESSLISLYKDWTF 616  
Db 535 HLSVTHPVKLLSHYRDTMTNALARQTLINAGGIFEMTVPGKFAIGMSAVVYKDWKF 594  
Qy 617 PQALPNMLKRGALVEDSSAPHGLRLLINDYPAVDGLDWSAIKTWVQDYCCLYYKDD 676  
Db 595 TEQGLPDDLIRGMAVEDPSSPKYRLLVSDYPYAADGLAIWHAIEQVSEYLAIVYPND 654  
Qy 677 NAVQNDFELQSWNELREKKGHADKKHEPWPMPKMTLSLBSCTTIIWIASALHAAVNF 736  
Db 655 GVLOQDTEVQAWKRETEVEGHCDLKDAPWPKMQSVPELAKACTIWIIGSALHAAVNF 714  
Qy 737 QYPCGYILNRPPTSRFRMPVEVGTAEYKELESNPEKAFRTICSELOALVSIISIELSK 796  
Db 715 QYVAGFLPNRPPTVSRFRMPFGTEEAELERDPERAFIHTISQIOTIIGVSLLEVLK 774  
Qy 797 HASDEVYLGORASIDWTSKIALAEKFKGNLFEVENRIMERNEKVNLRSGFVNLPY 856  
Db 775 HSSDELYLQDTEWTSDDKALEVFKFSPDRLEIYESKVGVGNHDPKRNNGPAKFPY 834  
Qy 857 TLLVPSSNE-----GLTGRGIPNSISI 878  
Db 835 MLLYPTNSDHTGQAEGLTARGIPNSISI 862

## RESULT 7

US-09-751-687-18  
; Sequence 18, Application US/09751687  
; Patent No. 6660915

; GENERAL INFORMATION:

; APPLICANT: Douma, Anneke

; APPLICANT: Doderer, Albert

; APPLICANT: Cameron-Mills, Verena

; APPLICANT: Skadhaug, Birgitte

; APPLICANT: Bech, Lene

; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY

; FILE REFERENCE: 11225.11US01

; CURRENT APPLICATION NUMBER: US/09/751.687

; CURRENT FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 18

; LENGTH: 864

; TYPE: PRT

; ORGANISM: Hordeum vulgare

US-09-751-687-18

Query Match

Best Local Similarity 51.9%; Score 2424; DB 4; Length 864;

Matches 470; Conservative 143; Mismatches 237; Indels 20; Gaps 9;

Qy 23 VINAGNLDLRVSSIGGNKIKGVKILMESNVLDTEPHSNLNDNFTLGGVSGFOLISA 82  
Db 1 MLGVGGIVSDLTGGIRGAHLKGSVVMKRNALDNDFGAHVMDGVTELLGRGVTCQLISS 60  
Qy 83 THT--SNDSRGKGVKNAYLERWL--TSIPPLFAGESVQINFQWD-ENFGPFPAGFIKNG 137  
Db 61 TNVDNHNNGRGKVGAEANLEQWLLPTNLFPFITNGENKFAVTFDWSVDKLGVPGAILVKN 120

Qy 138 HTSEFFLKSLTDDVPYGVGRVHFDNCNSWVYPSGRYKDKRIFPANHVLVPSQTPNPLRYR 197  
Db 121 HASEFFLKSLTLDNVPEGRGTIVFVANSWVYPOAKYRNVRFVANDTYLPHQMPAALPKYR 180  
Qy 198 EELANLWLDG-TGRKEWDRIDYVDVNDIADPDVGDHRPILGTTTEYPYPRRGTRGP 256  
Db 181 DDELRLNRDQDQGPYLDHDRVYRYDVVNDL-----GDSRDVLGGSKOLPYPRRCRTGRK 235  
Qy 257 RRRRDHNVSRISPTMSLDIYVVKDENFGLHKWSDFLGYTLKALSTSKPGQSIQFVTP 316  
Db 236 PSDSKPDHESRL-LLVQNVYVLRDELFGHLKQSDLLGYTLKGWLDGILAIRTYVDLSP 294  
Qy 317 NRPDNFKVDNLIPEFGPPIP-FNAFKTLTDTLTPFLFALVRNDGEKFLKFTPEVVKDN 375  
Db 295 GEFDSFADILKLYEGIKLPNIPALEEVRKRPPLQVLDLIPKGGDFLLKLPKPIIKVD 354  
Qy 376 KIGWSTDEEFAREMAGNPLIRLEAFPPSKLDENVYGNONSTITEEHIKHGLDGLT 435  
Db 355 QKAWMTDEEFAREMAGNPNMKLTTFPPKASTLDPSKYGDHTMTTEEHVAKLEGLT 414  
Qy 436 VDEAMQNRLYVDFHDMALPYLFRM-NATSTKTYATRTLLKDDGTLKPLVIELALPH 494  
Db 415 VQALAGNELYVQDHDNMLPELIDINLDASFVYATRTLLFLRGDGTLPVAILSP 474  
Qy 495 PGDDQLGAIKLYPFAENGVOKSIWOLAKAYVTVNDVGVHOLISHWLHVALEPPIATHR 554  
Db 475 IQELTAKSAVYTPPOHAGVEGWIMQKAYASVNDYGHQLISHWLHVALEPPIATHR 534  
Qy 555 HQQLSVLPHIHLKLYPHYKDTMFINASARQVLINANGLIETTHYPYSKYSMESSLISLYKDW 614  
Db 535 NQLSVTHPVYKLLSHYRDTMTNALARQTLINAGGIFEMTVPGKFAIGMSAVVYKDW 594  
Qy 615 TPDQALPNMLKRGALVEDSSAPHGLRLLINDYPAVDGLDWSAIKTWVQDYCCLYYK 674  
Db 595 NFTEQALPADLIRGMAVEDSAPHKVRLLINDYPAVDGLDWSAIAKQWVSDYITLYP 654  
Qy 675 DDNAVONDELOSWMNELREKKGHADKKHEPWPMPKMTLSLBSCTTIIWIASALHAAV 734  
Db 655 NQGVLOQDTEVQAWKRETEVEGHCDLKDAPWPKMQSVPELAKACTIWIIGSALHAAV 714  
Qy 735 FGQYPCGYILNRPPTSRFRMPVEVGTAEYKELESNPEKAFRTICSELOALVSIISIEL 794  
Db 715 FGQYPCGYILNRPPTSRFRMPVEVGTAEYKELESNPEKAFRTICSELOALVSIISIEL 774  
Qy 795 SKHASDEVYLGORASIDWTSKIALAEKFKGNLFEVENRIMERNEKVNLRSGFVNLP 854  
Db 775 SKHSDEVYLGQDTPAWTSDDKALEAFKFKGKLEKQVAVMNSDPLKRNRTGPAKF 834  
Qy 855 PYTLVPSSNE-----EGLTGRGIPNSISI 878  
Db 835 PYMLLYPTNSDHTGQAEGLTARGIPNSISI 864

## RESULT 8

US-09-061-768A-4

; Sequence 4, Application US/09061768A

; Patent No. 6204037

; GENERAL INFORMATION:

; APPLICANT: BRASH, ALAN R.

; APPLICANT: BOEGLIN, WILLIAM E.

; APPLICANT: JISAKA, MITSUO

; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARLES A. TAYLOR, JR.

; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

; CITY: DURHAM CAROLINA

; STATE: NORTH CAROLINA

; COUNTRY: USA

; ZIP: 27707

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

; COMPUTER: IBM PC/XT/AT compatible



Db 208 -----WRSUREMRRFL-----NFRKTPA 225  
QY 369 PEVVKDKIGNSTDEFAREMLAGNPLLIIRLEAPP-----TSKLDPNVYGNQNSTITE 424  
Db 226 AEYVFAH---WQDAFASQFLNGINPVLIERCHSLP-----NNFPVTDWMA 270  
QY 429 HGL-DGLTVDRAMKQNRILYVDFHDLMPYLTR-MNATSTKYATRTLL-LLKDDGTLKP 485  
Db 271 FVLGPGTSLQAELEKSGSLFLVD-FGILSGVHTNLNGKPOFSAAPMTLLHQSSGSGPLLP 329  
QY 486 LVIEL-ALPHPOGOLGAISKLYPPAENGVOKS-WOLAKAVTVVNDVGYHQLISHWLTH 544  
Db 330 IAIQLKQTPGPD-----NFIFLPSDDTWL---WLLAKTWVRNSEFYIHEAVTHLLAH 379  
QY 545 AVLPEFVIAHQRLSVLPHIHLVPHYKOTMFINASARQVLINANGLIB-TTHYPSKYS 603  
Db 380 LIPEVFALATLRLQPRCHPLFKLLIPHRYTLHINTLARELLVAPGKLIDKSLGTGGF 439  
QY 604 MELASILYKDWTFPDQALPNMLKRGGLAVEDSSAPHGLRLILINDYPFAVDGLDWSA 662  
Db 440 SLLIKRNEQUNYVLCUPEDIRARG--VED-----IPGYTRDDGMQIWAIGKS 487  
QY 664 WVQDYCCLYKDDNAVQNDFFELQSWNELREKKGHADKKHEPWPMPKMTLSLIESCTTII 723  
Db 488 FVSEIVSYPSDTSVQDDQLQAWREIPSEGFLGREGSGMPSSLDTREALVQYITWVI 547  
QY 724 WIASALHAANFGQYPVGYILNRPTTSRRRMPVGTAEYKELSNPEKAFRTICSELO 783  
Db 548 FTCSAKHAASVSGQFDSCVMWPNLPPTMQLPPT-----SKQARPE-SFIATLPVNS 600  
QY 784 ALVSIISIILSKHASDEVYLGORASIDWTS--KIALEAFKFGKNLFEVENRIMERK 841  
Db 601 SSYHTIALWLSASPGDQRLGHVDEFTEDAPRSVAAFQ---RKLIQISKGIRENR 657  
QY 842 EVNLKRGSPVNLPTLLVPSSNEGLTGRIENSI 878  
Db 658 -----GLALPYTYLDPL-----IENSVSI 677

## RESULT 10

US-09-547-435-2  
; Sequence 2, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides  
; FILE REFERENCE: 7705.0009-0000  
; CURRENT APPLICATION NUMBER: US/09/547,435  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-547-435-2

Query Match 10.4%; Score 484; DB 4; Length 711;

Best Local Similarity 25.5%; Pred. No. 2e-38;

Matches 163; Conservative 114; Mismatches 217; Indels 146; Gaps 21;

QY 306 PGLQSFIDVTPNEFDNFKVD-----NLPERGFP----- 334  
Db 151 PGFPCWVDV-----NSFQWESDKKFKALTCTTCVDQDSSGNRYLPGFPMKIDIPSLMY 205  
QY 335 -----IPFNAFKLTEDLTPLPKALVRNDGEKFL-----KFFT 368  
Db 206 MEPNVRYSATKTIIS-----LLFNAIPASLGMKRLGLLDRKSGWKLLDMDQNIWFCHKTFT 260

QY 369 PEVVKDKIGNSTDEFAREMLAGNPLLIIRLEAPP-----TSKLDPNVYGNQNSTITE 424  
Db 261 TKYVTEH---WCEDHFFGVYLVGNVPVNLHCISLPSKLPVNDWAPLLQDQTCLOTE 317  
QY 425 EHIKGLDGLTVDEAMKQNRILYVDFHDLMPYLTMKATSTKYATRTLLILKDDGTLK 484  
Db 318 -----LERGINFLADYWIILAEAPTHCLNGRQOYVAAPLCLLWLSQGALV 362  
QY 485 PLVIEIA-LPHPGQDQOLGAISKLYPPAENGVOKS-IWOLAKAVTVVNDVGYHQLISHWLHT 543  
Db 363 PLAIQLSQTPGPD-----SPIFLPTDS---EWDMLLAKTWVRNSEFLVHENNTFLCT 412  
QY 544 HAVLPEFVIAHQRLSVLPHIHLVPHYKOTMFINASARQVLINANGLIB-TTHYPSKY 602  
Db 413 HLLCEAFAMATLRLQPLCHPIYKLLPHTRYTLQVNTIARATLLNPEGLVQVTSIGRQG 472  
QY 603 SMELASILYKDWTFPDQALPNMLKRGGLAVEDSSAPHGLRLILINDYPFAVDGLDWSA 662  
Db 473 LYLIMSTGLAHYTYNFCPLPSLRGV-----LAIPNHYRDDGLKIWAILE 520  
QY 663 TWQDYCCLYKDDNAVQNDFFELQSWNELREKKGHADKKHEPWPMPKMTLSLIESCTTII 722  
Db 521 SFVSEIVGYYPDSASVQDDSELQAWTGEIFAQAFLGREGSGFPRLCTPGEMVRFELTAI 580  
QY 723 WIASALHAANFGQYPVGYILNRPTTSRRRMPVGTAEYKE-LESNPEKAFRTICS 780  
Db 581 IFNCSAQHAANVSGQHDGFMWPNAPSSWRQPPQTKGTTILKTYLDLPE---VNISCN 637  
QY 781 ELQALVSIISIILSKHASDEVYLGORASIDWTS--KIALEAFKFGKNLFEVENRIME 838  
Db 638 NL-----LLFVLSQEPKQDQRLGTYPDHFTEDAPRSVAAFQ---SRLAQISRDIOE 688  
QY 839 RKEVNLKRGSPVNLPTLLVPSSNEGLTGRIENSI 878  
Db 689 RNQ-----GLALPYTYLDPL-----IENSVSI 711

## RESULT 11

US-09-547-435-24  
; Sequence 24, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides  
; FILE REFERENCE: 7705.0009-0000  
; CURRENT APPLICATION NUMBER: US/09/547,435  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 867  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-547-435-24

Query Match 10.4%; Score 484; DB 4; Length 867;

Best Local Similarity 25.5%; Pred. No. 2.8e-38;

Matches 163; Conservative 114; Mismatches 217; Indels 146; Gaps 21;

QY 306 PGLQSFIDVTPNEFDNFKVD-----NLPERGFP----- 334  
Db 307 PGFPCWVDV-----NSFQWESDKKFKALTCTTCVDQDSSGNRYLPGFPMKIDIPSLMY 361  
QY 335 -----IPFNAFKLTEDLTPLPKALVRNDGEKFL-----KFFT 368  
Db 362 MEPNVRYSATKTIIS-----LLFNAIPASLGMKRLGLLDRKSGWKLLDMDQNIWFCHKTFT 416





STRANDEDNESS: single  
TOPOLOGY: unknown  
US-09-061-768A-2

Query Match 10.1%; Score 473; DB 3; Length 676;  
Best Local Similarity 24.8%; Pred. No. 2.2e-37;  
Matches 185; Conservative 114; Mismatches 261; Indels 186; Gaps 30;  
QY 153 PGYGRVHDCNSWYPSG---RYKKDRIFFAHVLPSPQTPNP-LRKYYEELMNLRGD 207  
DB 97 PRGCHLLPFCYQWLEGAGTLVLQEGTAKVSWADH-----HPVLOQQRQBEL----- 142  
QY 208 GTGERKEWDRIYDVIYNDIADPDVGDHRPILGTTGTEYPPRRGRTGRPSRRDHYESR 267  
DB 143 --QARQE---MYQWKAYNP-GWPHCLDEKTV-----RKGL-----WRLNEMKR 215  
QY 268 LSPIMSLDIYVPKDNFCHLKMDSFLGYTLKALSISIKPGIQLSIFDVTPEFDFNKEVDN 327  
DB 176 YSTAKNANFYLOQSAFAEMKIKGLD-----RKGL-----WRLNEMKR 215  
QY 328 LFE-RGFFPIPPNFKLTEDLTPFLFKALVRNDGKFLKFTPEVVKONKIGWSTDEEPA 386  
DB 216 IFNFRTPAAEHAFAE-----HWQEDAPFA 239  
QY 387 REMLAGNPILLIRLEAPPTSKLDPNVYGNQNSITTEHIXHGL-DGLTVDEAMKQNEL 445  
DB 240 SQFLMGNPVLIRRHCHYLP-----KNFPVTDAWVASLGGPSTSLQAELEKGL 287  
QY 446 YIVDFHDMALPILTR-MNATSTKTVATRLTLLKDD-GTLKPLVIELA-LPHPOGQDLGA 502  
DB 288 FLVD-HGILSGIQTNVINGKQFSAAPMTLLYQSPGCGPLPLAIQLSQTGPN----- 340  
QY 503 ISKLYFPAENGVOQSIWOLAKAYTVNDVGVHQLISHWLHVALEPFIATHRQSLVHL 562  
DB 341 -SPIFLPTDD---KWDWLLAKTWVRNAEFSFHEALTHLLSHLLPEVFTLATLRLQHPCH 396  
QY 563 PIHKLIVPHYKDTMFINASARQVLINANGILIE-TTHYPSKYSMELSILYKDWTFPPQAL 621  
DB 397 PLFKLLIPTHRYTLHINTLARELLIVPGQVDRSTGIGEGFSELLQRMKQNLNLSLCL 456  
QY 622 PNNLMKRGVAVDSAPHLKRLINDYFPAVDGLDIWSAIAKTWQDYCYCLLYKDDNAVQN 681  
DB 457 PEDIRTRG--VED-----IPGYYYRDDGMQINGAVERFVSEIIGIYPSDESVDQ 504  
QY 682 DFLQSWNELREKGHADKHEPWPWKMTLSIELIESCTTIIWIASALHAANFGQVPEYG 741  
DB 505 DRELOAWREIFSKGFLNQESSGIPSSLETREALVOYVTWVIFCSAKHAASVAGQFDS 564  
QY 742 GYILNRPSTTSRRFMPE---VGTAEYKELESNPEKAFNLTI-----CSELOALVSIIE 792  
DB 565 AMWPNLPSPMQLPPTPSKGLATCE-----GFIALPPVNATCDVIAL-----W 608  
QY 793 ILSKHASDEVILQOASIDWTSKIALFAFEKFGKNLFEVENRIMERKENVLNKNSGPV 852  
DB 609 LLSEKFGQORPUGTYPDSEHFT-EAPRPSIATFOSRLAQISRGIOERNR-----GLV 659  
QY 853 NLPYTLVPSNNEGLTGRGIPNSISI 878  
DB 660 -LPYTYLDPPL-----IENSUSI 676

## RESULT 14

US-09-764-246-2  
Sequence 2, Application US/09764246  
Patent No. 6649355

## GENERAL INFORMATION:

APPLICANT: BRASH, ALAN R.  
BOEGLIN, WILLIAM E.  
JISAKA, MITSUO

TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.

STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/764,246  
FILING DATE: 17-Jan-2001  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 676 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-764-246-2

Query Match 10.1%; Score 473; DB 4; Length 676;  
Best Local Similarity 24.8%; Pred. No. 2.2e-37;  
Matches 185; Conservative 114; Mismatches 261; Indels 186; Gaps 30;

QY 153 PGYGRVHDCNSWYPSG---RYKKDRIFFAHVLPSPQTPNP-LRKYYEELMNLRGD 207  
DB 97 PRGCHLLPFCYQWLEGAGTLVLQEGTAKVSWADH-----HPVLOQQRQBEL----- 142  
QY 208 GTGERKEWDRIYDVIYNDIADPDVGDHRPILGTTGTEYPPRRGRTGRPSRRDHYESR 267  
DB 143 --QARQE---MYQWKAYNP-GWPHCLDEKTV-----EDLELNK 175  
QY 268 LSPIMSLDIYVPKDNFCHLKMDSFLGYTLKALSISIKPGIQLSIFDVTPEFDFNKEVDN 327  
DB 176 YSTAKNANFYLOQSAFAEMKIKGLD-----RKGL-----WRLNEMKR 215  
QY 328 LFE-RGFFPIPPNFKLTEDLTPFLFKALVRNDGKFLKFTPEVVKONKIGWSTDEEPA 386  
DB 216 IFNFRTPAAEHAFAE-----HWQEDAPFA 239  
QY 387 REMLAGNPILLIRLEAPPTSKLDPNVYGNQNSITTEHIXHGL-DGLTVDEAMKQNEL 445  
DB 240 SQFLMGNPVLIRRHCHYLP-----KNFPVTDAWVASLGGPSTSLQAELEKGL 287  
QY 446 YIVDFHDMALPILTR-MNATSTKTVATRLTLLKDD-GTLKPLVIELA-LPHPOGQDLGA 502  
DB 288 FLVD-HGILSGIQTNVINGKQFSAAPMTLLYQSPGCGPLPLAIQLSQTGPN----- 340  
QY 503 ISKLYFPAENGVOQSIWOLAKAYTVNDVGVHQLISHWLHVALEPFIATHRQSLVHL 562  
DB 341 -SPIFLPTDD---KWDWLLAKTWVRNAEFSFHEALTHLLSHLLPEVFTLATLRLQHPCH 396  
QY 563 PIHKLIVPHYKDTMFINASARQVLINANGILIE-TTHYPSKYSMELSILYKDWTFPPQAL 621  
DB 397 PLFKLLIPTHRYTLHINTLARELLIVPGQVDRSTGIGEGFSELLQRMKQNLNLSLCL 456  
QY 622 PNNLMKRGVAVDSAPHLKRLINDYFPAVDGLDIWSAIAKTWQDYCYCLLYKDDNAVQN 681  
DB 457 PEDIRTRG--VED-----IPGYYYRDDGMQINGAVERFVSEIIGIYPSDESVDQ 504



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2004, 11:33:03 ; Search time 25.4756 Seconds  
(without alignments)  
1794.561 Million cell updates/sec

Title: US-09-937-908-1  
Perfect score: 4675  
Sequence: 1 MFGIGKNIIEGALTGTGLA.....LVPSNBLTGRGIPNSISI 878

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2955	63.2	860	1 LOXA LYCES	P38415 lycopersico
2	2932	62.7	861	1 LOX1 SOLTU	P37811 solanum tub
3	2847	60.9	859	1 LOX1 ARATH	Q06327 arabidopsis
4	2812.5	60.2	859	1 LOXB LYCES	P38416 lycopersico
5	2769	59.2	857	1 LOX3 SOYEN	P09186 glycine max
6	2705.5	57.9	864	1 LOX2 PEA	P09918 pisum sativ
7	2696.5	57.7	861	1 LOX3 PEA	P09439 glycine max
8	2690	57.5	865	1 LOX2 SOYEN	P24095 glycine max
9	2644.5	56.6	864	1 LOX3 SOYEN	P27480 phaseolus v
10	2596	55.5	862	1 LOXA PHAVU	P38417 glycine max
11	2591	55.4	853	1 LOX4 SOYEN	P08170 glycine max
12	2582.5	55.2	839	1 LOX1 SOYEN	P38414 lens culina
13	2546	54.5	866	1 LOX1 LENCU	P29114 hordeum vul
14	2438	52.1	862	1 LOX1 HORVU	P27481 phaseolus v
15	2415	51.7	741	1 LOXB PHAVU	P29250 oryza sativ
16	2390.5	51.1	865	1 LOX2 ORYSA	P38418 arabidopsis
17	1740	37.2	896	1 LOXC ARATH	Q89sm2 hordeum vul
18	1665	35.6	896	1 LX23 HORVU	P38419 oryza sativ
19	1656	35.4	923	1 LOXC ORYSA	P39184 hordeum vul
20	1532.5	32.8	936	1 LX21 HORVU	Q89sm3 hordeum vul
21	1508	32.3	932	1 LX22 HORVU	O16025 pleura ho
22	569	12.2	1066	1 AOSL PLEHO	P09917 homo sapien
23	516.5	11.0	673	1 LOX5 HUMAN	P48999 mus musculu
24	515.5	11.0	673	1 LOX5 MOUSE	P51399 mesocricetu
25	510	10.9	672	1 LOX5 MESAU	P55249 mus musculu
26	500	10.7	662	1 LOXE MOUSE	Q9wv07 mus musculu
27	498.5	10.7	711	1 LX3B MOUSE	Q35936 mus musculu
28	495.5	10.6	677	1 LX1B MOUSE	P12527 rattus norv
29	495	10.6	672	1 LOX5 RAT	Q9byj1 homo sapien
30	484	10.4	711	1 LX3B HUMAN	O15296 homo sapien
31	473	10.1	676	1 LX1B HUMAN	O15043 oryctolagus
32	469	10.0	662	1 LOXP RABIT	P39654 mus musculu
33	466	10.0	662	1 LOXL MOUSE	

#### RESULT 1

ID	LOXA LYCES	STANDARD;	PRT;	860 AA.
AC	P38415;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Lipoxygenase A (EC 1.13.11.12).			
GN	LOX1.1 OR LOXA.			
OS	Lycopersicon esculentum (Tomato).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	lamiales; Solanales; Solanaceae; Solanum.			
OX	NCBI_TaxID=4081;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Caruso; TISSUE=Pericarp;			
EX	MEDLINE=95062736; PubMed=7972514;			
RA	Perrie B.J., Beaudoin N., Burkhardt W., Bowsher C.G., Rothstein S.J.;			
RT	"The cloning of two tomato lipoxygenase genes and their differential expression during fruit ripening."			
RL	Plant Physiol. 106:109-118(1994).			
CC	-1- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING A CIS, CIS-1,4-PENTADIENE STRUCTURE.			
CC	-1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-hydroperoxyoctadeca-9,11-dienoate.			
CC	-1- COFACTOR: Iron, one atom tightly bound per molecule.			
CC	-1- SUBUNIT: Monomer (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN GERMINATING SEEDS AS WELL AS IN RIPENING FRUIT.			
CC	-1- SIMILARITY: Belongs to the lipoxygenase family.			
CC	-1- SIMILARITY: Contains 1 PLAT domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
CC	EMBL; U09026; AAAS3184.1; --			
DR	HSPSP; P08170; 2SBL.			
DR	InterPro; IPR000907; Lipoxygenase.			
DR	InterPro; IPR01024; Lipoxygenase_LH2.			
DR	InterPro; IPR008976; PLAT_LH2.			
DR	Pfam; PF00305; Lipoxygenase; 1.			
DR	Pfam; PF01477; PLAT; 1.			
DR	PRINTS; PR00087; LIPOXYGENASE.			
DR	SMART; SM00308; LH2; 1.			
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.			
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.			

#### ALIGNMENTS

P12530 oryctolagus  
O70582 mus musculu  
O75342 homo sapien  
P16469 sus scrofa  
P27479 bos taurus  
P18054 homo sapien  
P39655 mus musculu  
Q02759 rattus norv  
P16050 homo sapien  
P42782 haemophilus  
P56785 arabidopsis  
P30195 staphylococ

34 463.5 9.9 662 1 LOX1 RABIT  
35 459 9.8 701 1 LOXR\_MOUSE  
36 457.5 9.8 701 1 LOXR\_HUMAN  
37 453 9.7 662 1 LOXP\_FIG  
38 443 9.5 662 1 LOXP\_BOVIN  
39 441.5 9.4 662 1 LOXP\_HUMAN  
40 435 9.3 662 1 LOXP\_MOUSE  
41 433 9.3 662 1 LOX2 RAT  
42 427.5 9.1 661 1 IGAL\_HAELN  
43 135.5 2.9 1541 1 YCF1\_ARATH  
44 125 2.7 1786 1 YCF1\_ARATH  
45 119 2.5 986 1 EPIB\_STAEP









Db 4 GGIWDAL--LGKDRPKVKGRVILMKKNVLDIFINIGASVVDIGSIDLLQKQVSIQLISGSV 61  
QY 85 TSNSRGRVGNKAYLERLWLTISIPLPAGESVFQNFQWD-ENFGPGAFRIKNGHTSEFF 143  
Db 62 NYDGLGKLSPAYLESWLTITITAGESVTFVDFWDRDEFVPGAFIKNLHLEFF 121  
QY 144 LKSLTLDVPGVGRVHPCNSWVPSGRYKXDRIFFAHNVLPSTPNLRKREELWN 203  
Db 122 LKSLTLEDVPGVGRVHPCNSWVPSGRYKXDRIFFAHNVLPSTPNLRKREELWN 181  
QY 204 LRGGTGERKEDWTDYDNDIADPDVGH--RPIILGTTTEYPRRGTCPRERD 261  
Db 192 LRGGTGERKEDWTDYDNDIADPDVGH--RPIILGTTTEYPRRGTCPRERD 241  
QY 262 HNYEELSLPMSLDIYVPRDERFGRVKSDFLTSSKSLQTLPAFKALCNTPFENS 301  
Db 242 PNCESRNLPLMSLDIYVPRDERFGRVKSDFLTSSKSLQTLPAFKALCNTPFENS 301  
QY 322 PKEVDNLERGFPPFNAP-KTLTDLTPPLFKALVRNDGKFLKPTPEVVKDKNLGS 380  
Db 302 FADVLNLVGGIKLPEGPWLKAITDNTSSEIKDILQTDGGLKYPPTQVIOGDKTAWR 361  
QY 381 TDEEFARMLAGNPLIRLEAPPTSKLPDENVGNQNSTITEHKKHGLDGLTVDEAM 440  
Db 362 TDEEFARMLAGNPLIRLEAPPTSKLPDENVGNQNSTITEHKKHGLDGLTVDEAM 421  
QY 441 KQRLYIVDFHMLPMTYTRWN-ATSTKYATRLLKDDGTLKPLVIELALPHQGDQ 499  
Db 422 KSNRLFINHHDIVMPLLRKINMGSANTKAYASRTLLFLQDDTLKPLAELSLPHPDQDQ 481  
QY 500 LGATSKLPFAENGVSIMOLAKAYVTNDVGVHQLTSHWLHVALEPVIATHROLS 559  
Db 482 FGVSKVTADQGVGSIWQFPAKAVAVNDMGHQLISHWLNTHAVIEPVPVATNRHLS 541  
QY 560 VLPHIHLKLVPHYKDTMFINASRQVLINANGLIETTHYPSKYSMELSSILYKDWTFPDQ 619  
Db 542 VLPHIHLKLVPHYKDTMFINASRQVLINANGLIETTHYPSKYSMELSSILYKDWTFPDQ 600  
QY 620 ALPNLMKSGLAVEDSSPHGLRLINDYPANVGLDIWSAIIKTVQDYCLLYKDNVAV 679  
Db 601 ALPADLKRGAVEDSSPHGLRLINDYPANVGLDIWSAIIKTVQDYCLLYKDNVAV 660  
QY 680 QNDPELQSWNELREKGHADKHPFMPKMTLSIELIESCTTIITWIASALHAANFQYFP 739  
Db 661 EKDTLOAWKRELREEGHGDKDEAWPKLQTRQELRDCCTIITWIASALHAALHFLYS 720  
QY 740 YGYILNPTTSRRPMPVGAETAEKLESNEPEKAPLRTICSELAQVSIHIEILSKHAS 799  
Db 721 YAGYLPNPTLSCLNMPPEGVSEYELKTNPKVFLKTFVPLQSLSEISIFVSSRHAS 780  
QY 800 DEVYLGQASIDWTSKLTALBAFKFKNLPEVENRWERKEVNLKRNRPVNLPTLL 859  
Db 781 DEVYLGQASIDWTSKLTALBAFKFKNLPEVENRWERKEVNLKRNRPVNLPTLL 840  
QY 860 VPSNNEGTLGRGIPNSISI 878  
Db 841 PPTSEGLTKGIPNSVSI 859

RESULT 5  
LOX3\_SOYBN STANDARD; PRT; 857 AA.  
AC F09186; Q39838;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Seed lipoxigenase-3 (EC 1.13.11.12) (u-3).  
GN LOX1.3 OR LOX3.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;

RN SEQUENCE FROM N.A.  
RP Yenofsky R.L.; Fine M., Liu C.;  
RA Isolation and characterization of a soybean (Glycine max)  
RT lipoxigenase-3 gene.;  
RL Mol. Gen. Genet. 211:215-222(1988).  
RN REVISIONS.  
RP Yenofsky R.L.;  
RA Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.  
RN SEQUENCE FROM N.A., AND MUTAGENESIS OF ASN-713.  
RP STRAIN=cv. Provar;  
RX MEDLINE=95092758; PubMed=7999759;  
RA Kramer J.A., Johnson K.R., Dunham W.R., Sands R.H., Funk M.O. Jr.;  
RT "Position 713 is critical for catalysis but not iron binding in  
soybean lipoxigenase 3";  
RL Biochemistry 33:15017-15022(1994).  
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
RP STRAIN=cv. Provar;  
RX MEDLINE=97440646; PubMed=9294864;  
RA Skrzypczak-Jankun E., Anzel L.M., Kroa B.A., Funk M.O. Jr.;  
RT "Structure of soybean lipoxigenase L3 and a comparison with its  
L1 isoenzyme";  
RL Proteins 29:15-31(1997).  
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RP STRAIN=cv. Provar;  
RX MEDLINE=99119225; PubMed=9922163;  
RA Pham C., Jankun J., Skrzypczak-Jankun E., Flowers R.A., Funk M.O. Jr.;  
RT "Structural and thermochemical characterization of lipoxigenase-  
catechol complexes";  
RL Biochemistry 37:17952-17957(1998).  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RP STRAIN=cv. Provar;  
RX MEDLINE=21547069; PubMed=11686682;  
RA Skrzypczak-Jankun E., Bross R.A., Carroll R.T., Dunham W.R.,  
RA Funk M.O. Jr.;  
RT "Three-dimensional structure of a purple lipoxigenase";  
RL J. Am. Chem. Soc. 123:10814-10820(2001).  
CC -1- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF  
DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND  
DEVELOPMENT, PEST RESISTANCE, AND SENSATION OR RESPONSES TO  
WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING  
A CIS, CIS-1,4-PENTADIENE STRUCTURE.  
CC -1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-  
hydroperoxyoctadeca-9,11-dienate.  
CC -1- COFACTOR: Iron, one atom tightly bound per molecule.  
CC -1- SUBUNIT: Monomer.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,  
L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT  
ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.  
CC -1- SIMILARITY: Belongs to the lipoxigenase family.  
CC -1- SIMILARITY: Contains 1 PLAT domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; X56928; CAA30016.1; -  
DR EMBL; X13302; CAA31664.1; ALT\_SEQ.  
DR EMBL; USC081; AAB41272.1; -  
DR PDB; 1LNH; 29-MAR-96.  
DR PDB; 1N03; 03-JUN-03.  
DR PDB; 1IK3; 14-NOV-01.  
DR InterPro; IPR000907; lipoxigenase.

DR InterPro; IPR001024; Lipoxigenase\_LH2.  
 DR InterPro; IPR008976; PLAT\_LH2.  
 DR Pfam; PF00305; lipoxigenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXIGENASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXIGENASE\_1; 1.  
 DR PROSITE; PS00081; LIPOXIGENASE\_2; 1.  
 DR PROSITE; PS00955; PLAT; 1.  
 KW Oxidoreductase; Dioxigenase; Iron; Multigene family; 3D-structure.  
 FT DOMAIN 38 163  
 FT METAL 518 518  
 FT METAL 523 523  
 FT METAL 709 709  
 FT METAL 857 857  
 FT METAL 857 857  
 FT VARIANT 25 25  
 FT VARIANT 57 57  
 FT VARIANT 112 112  
 FT VARIANT 112 112  
 FT VARIANT 201 201  
 FT VARIANT 382 382  
 FT VARIANT 428 428  
 FT VARIANT 630 630  
 FT MUTAGEN 713 713  
 FT N->A,S: NO LOSS OF IRON-BINDING; LOSS OF CATALYTIC ACTIVITY.  
 FT MUTAGEN 713 713  
 FT N->H: NO LOSS OF IRON-BINDING; NO CHANGE IN CATALYTIC ACTIVITY.  
 FT STRAND 11 20  
 FT HELIX 21 24  
 FT TURN 26 28  
 FT HELIX 29 31  
 FT HELIX 50 54  
 FT TURN 55 57  
 FT STRAND 58 64  
 FT STRAND 76 81  
 FT STRAND 85 86  
 FT TURN 89 91  
 FT TURN 94 95  
 FT STRAND 96 104  
 FT TURN 107 109  
 FT STRAND 112 119  
 FT STRAND 125 133  
 FT STRAND 141 149  
 FT STRAND 151 151  
 FT HELIX 152 154  
 FT STRAND 159 162  
 FT TURN 169 171  
 FT HELIX 174 188  
 FT TURN 197 198  
 FT STRAND 204 205  
 FT STRAND 207 207  
 FT HELIX 213 215  
 FT HELIX 217 219  
 FT STRAND 224 224  
 FT STRAND 235 236  
 FT STRAND 242 242  
 FT STRAND 248 248  
 FT TURN 250 250  
 FT TURN 260 261  
 FT HELIX 273 282  
 FT TURN 283 283  
 FT HELIX 284 293  
 FT STRAND 304 308  
 FT HELIX 309 311  
 FT STRAND 315 315  
 FT HELIX 319 322  
 FT TURN 323 325  
 FT TURN 329 330  
 FT STRAND 336 337  
 FT STRAND 343 344  
 FT HELIX 349 351  
 FT HELIX 357 359  
 FT HELIX 361 370

FT STRAND 379 379  
 FT STRAND 386 386  
 FT TURN 391 394  
 FT STRAND 398 398  
 FT TURN 403 404  
 FT HELIX 415 420  
 FT TURN 421 422  
 FT STRAND 424 428  
 FT TURN 431 433  
 FT HELIX 434 440  
 FT TURN 441 444  
 FT STRAND 450 456  
 FT TURN 458 459  
 FT STRAND 462 472  
 FT TURN 474 475  
 FT STRAND 481 486  
 FT HELIX 492 520  
 FT TURN 521 522  
 FT HELIX 523 536  
 FT TURN 539 540  
 FT HELIX 542 547  
 FT HELIX 548 551  
 FT TURN 552 553  
 FT HELIX 554 564  
 FT TURN 565 565  
 FT TURN 568 569  
 FT HELIX 571 575  
 FT TURN 577 578  
 FT HELIX 579 581  
 FT HELIX 582 590  
 FT TURN 591 592  
 FT HELIX 595 598  
 FT HELIX 600 606  
 FT TURN 607 608  
 FT STRAND 610 612  
 FT TURN 614 615  
 FT TURN 617 618  
 FT STRAND 620 622  
 FT TURN 625 626  
 FT HELIX 628 649  
 FT TURN 650 651  
 FT HELIX 655 659

Query Match 59.2%; Score 2769; DB 1; Length 857;  
 Best Local Similarity 60.0%; Pred. No. 5e-181;  
 Matches 521; Conservative 132; Mismatches 184; Indels 32; Gaps 7;

QY 28 GNILDRVSSLGNGKIKGVILMRSNVLDPTEFHS-----NLLDNFTLGGG 74  
 DB 3 GGLLHR-----CHKIKGTIVLMRKVNLHVNSVTSVGGIIGQGLDLVGSTLDTLTAFLGRP 57  
 QY 75 VSFQLISATHSTNSDRGKVGKAYLERWLTISIPPLFAGESVFQINFQDENFGPPEAFPI 134  
 DB 58 VSLQLISATKADANGKGLKATFLEGIITSLTLCAGQSAFKINFENDGSGILGAFYI 117  
 QY 135 KNGHTSEPLKSLTLDVPGYGRVHFDCNSWYPSGRYKDRIFPANHVYLPSPQPNPLR 194  
 DB 118 KNFMQTEFFLVSLTLEDIPNHGSIHFVCSWITYNAKLFKSDRIFPANQTYLPSETPAPLV 177  
 QY 195 KYREBELNLRGDTGERKEWDRIYDYVDYNDIADPDVGDH--REILGGTTEYPYPRGR 252  
 DB 178 KYREBELNLRGDTGERKEWERYDYVDYNDLGDGDKGENHARVLCGNDTFFPYPRGR 237  
 QY 253 TGRPRSRDHNYESRLSPIMSLDIYVPKDFHGLKMSDFLGYTLKALSIKPLQSIPI 312  
 DB 238 TGRKPTRKDPNSESR-----SNDVYLPRDEAFGLKSSDFLTGLKSVSNVLPLOSAF 292  
 QY 313 DV--TPNSFDNPKFYDNLFERGFPFPFNAFKTLTDLTP-PLFKALVENDGCKFLKFPPT 369  
 DB 293 DLNFTPRFPDSFDEVHGLYSGIKLPTD-----ITSKISPLVLKFIPTDGEQALKFPFP 346  
 QY 370 EYVKONKIGWSTDEBFAREMLAGPNPLIRLEAPPTSKLDPNVYGNQNSTITBEHIKH 429

Db 349 KVIQVSKSAMWTDDEFAREMLAGVNPINLIRCIKBPFRPSKLDQVYGDHTSQITKEHLEP 408

QY 430 GLDGLTVDEAMKONKLYIVDFHDALMPYLTRMNTATSTKYATRILLKLDGTLKPLVIE 489

Db 409 NLEGLTVDEATQNKELFLGHDPMPYLRINATSTKAYATRILFLKNDGTLRPLAIE 468

QY 490 LALPHQDQDQGAISKLFPBAENGQVKSISWOLAKAYVTVDVGYHQLISHWLTHAVLEP 549

Db 469 LSLPHQDQDQGAISKLFPBAENGQVKSISWOLAKAYVTVDVGYHQLISHWLTHAVLEP 528

QY 550 FVIATHROLVSLPHLTHKLLVHYKDTMEINASQVNLINANGLIETTHYPKSYKSWELSSI 609

Db 529 FIATNRHLSVHPYIKLLHYRDTMNINGLRLSLVNDGGVIEQTLWGRYSVENSAY 588

QY 610 LYKDWTFDQALPNNIMKRGSLAVEDSSAPHGRLRLIINDYPFVAVDGLDITSAIKTWVODYC 669

Db 589 YKDWVFTDQALPADLIRKGMALIEDPSCPHGRLVIEDYPVAVDGLDITSAIKTWVODYC 648

QY 670 CLYKDDNAVQNDPELOQWNLREKKGADKHPHWPWPKMOTLSBELIESCTTIWIASAL 729

Db 649 FLYKSDDTLREDPELOQWNLREKKGADKHPHWPWPKMOTLSBELIESCTTIWIASAL 708

QY 730 HAAVNFQYPGYGLIINPTTSRRFMPVGTAEYKELESNEPEKAFRTICSELQALYSIS 789

Db 709 HAAVNFQYPGYGLIINPTTSRRFMPVGTAEYKELESNEPEKAFRTICSELQALYSIS 768

QY 790 IIEILSKHASDEVYLGQASIDWTSKIALFAEFKFGKNLFEVENRIMERKYNLKNRS 849

Db 769 VIEILSKHASDEVYLGQASIDWTSKIALFAEFKFGKNLFEVENRIMERKYNLKNRS 828

QY 850 GPVNLPTLLVPSNNEGTLGRGIPNSISI 878

Db 829 GPVQMPYTLILPSSKEGLTFRGIPNSISI 857

RESULT 6

ID LOX2\_PEA STANDARD; PRT: 864 AA.

AC P14856;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Seed lipoxigenase-2 (EC 1.13.11.12).

GN LOX1.2.

OS *Pisum sativum* (Garden pea).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; *Pisum*.

OX NCBI\_TaxID=3888;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=cv. Birte.

RX MEDLINE=90147555; PubMed=2515855;

RA Ealing P.W.; Casey R.;

RT "The cDNA cloning of a pea (*Pisum sativum*) seed lipoxigenase.

RT Sequence comparisons of the two major pea seed lipoxigenase

RT isoforms.";

RL Biochem. J. 264:929-932 (1989).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Birte;

RA Casey R.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBSJ databases.

CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF

CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND

CC DEVELOPMENT, PEST RESISTANCE, AND SENSENCE OR RESPONSES TO

CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING

CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-

CC hydroperoxyoctadeca-9,11-dienoate.

CC -!- COFACTOR: Iron.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the lipoxigenase family.

CC -!- SIMILARITY: Contains 1 PLAT domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL; X17061; CAA34906.1; -.

DR EMBL; X78580; CAA55318.1; -.

DR PIR; S07075; S07075.

DR HSP; P08170; 2SBL.

DR InterPro; IPR000907; Lipoxigenase.

DR InterPro; IPR001024; Lipoxigenase\_LH2.

DR InterPro; IPR008976; PLAT\_LH2.

DR Pfam; PF00305; lipoxigenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PR00087; LIPOXYGENASE.

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.

DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.

DR PROSITE; PS00095; PLAT; 1.

KW Oxidoreductase; Dioxigenase; Iron; Multigene family.

FT DOMAIN 46 171

FT METAL 524 524 IRON (BY SIMILARITY).

FT METAL 529 529 IRON (BY SIMILARITY).

FT METAL 716 716 IRON (BY SIMILARITY).

FT METAL 864 864 IRON (BY SIMILARITY).

FT CONFLICT 333 333 L -> I (IN REF. 2).

FT CONFLICT 562 562 MISSING (IN REF. 2).

FT CONFLICT 578 578 L -> I (IN REF. 2).

SQ SEQUENCE 864 AA; 97133 MW; 2919AF5FAP272CDF CRC64;

Query Match 57.9%; Score 2705.5; DB 1; Length 864;

Best Local Similarity 59.9%; Pred. No. 11e-176; Indels 33; Gaps 7;

Matches 517; Conservative 119; Mismatches 194;

QY 39 GNKIKGVILMRSNVLDTFEHS-----NLLDNFTLLGGVYFQI 80

Db 12 GHKIRGTVMKRVLDFTNIVSIGGNVGVIDSGINIGSTLDGLTAFIAGRSVSLQI 71

QY 81 SATHTSNDSRGKGNKAYLERWLTSTPLPAGESVYQINFDENFGPGAFIKNGHTS 140

Db 72 SATKSANGKGVKGDFTFLEGVLASLTLAGESAFNTHFWDHENGIPGAFYIKNYQV 131

QY 141 EFFKLSLTDDVPYGRVHFDGNSWYPSGRYKDRIFANHVYLPSTPNLRKYREE 200

Db 132 EFFKLSLTLEDVPHGCTIRFCVNSWYNSKLYKSPRIIFANKSLPSETPSLVKYREE 191

QY 201 LWNLRDGTGERKWDRIYDYVNDIADPDVGDH--RPILGGTTEYPYPRGRTRGRPS 258

Db 192 LQTLRGDGTGERKHLHERIYDYVNDLGNPDHGEHLARPILGSSSTHPYPRGRTRYPT 251

QY 259 RDHNVESSLSPITMSLDIYVPDENFGLKMSDFGLYTLKALSIKPLQSIQFV--TP 316

Db 252 RQDPNSEK-----PATETVYPRDENFGLKMSDFGLYTLKALSIKPLQSIQFV 306

QY 317 NEFDNFKVDNLFERGFPIPFNAFKTLTDLTPPFLKALVRNDGKFKLPFPTEVVKONK 376

Db 307 NEFDSFDQVRLNFEQGIKPLDVI STLSPVVKBIFRDTGQVQLKFTPPHVRVSK 363

QY 377 IGWSTDEEFAREMLAGNPLLRLEAPPTSKLPDNYVGNQNSITTEHIKHGDGLTV 436

Db 364 SAWMTDEEFAREMLAGNPMIRGQEPFPKKNLDPAEYGDHTSKISVDVL--NLDGCTI 421

QY 437 DEAMKONRLIYVDFHDALMPYLTRMNTATSTKYATRILLKLDGTLKPLVIELPHQ 496

Db 422 DEALASGRFLDYHDTFIPFLRRINETSAKAYATRTILFLKENGTLKPAVLELSLPHD 481

QY 497 GQOLGAISKLYPBAENGVOKSWOLAKAYVTVDVGYHQLISHWLTHAVLEPFIATHR 556

Db 482 GDKSGFVSKVILPADEGVESTIWLAKAYVVVNDSCYHQLMSHLNTHAVIEPVIATNR 541  
 Qy 557 QLSVLHPHTKLVPHVKTMP- INASARQVLINANGLETTHYPSKYSMELSSLYKDW 615  
 Db 542 QUSVHPINKLAPHYRDTMMINALARDSLINANGLIERSFLSKYAVEMSSAVYKVV 601  
 Qy 616 PPDQALPNMLMKRGIAVEDSSAPHGLRLINDYPAVDGLDIWAIAKTTWQDYCCLYYKD 675  
 Db 602 FTDQALPNDLIKRNMAVSSSPYGLRLIEDYPVAVDGLBIWTAIKTTWQDYVSLYAT 661  
 Qy 676 DNAVONDELQSWNELKREKADKHEPMPKOTLSELIESCTTIWIASALHAANVF 735  
 Db 662 DNDIKNDSELOHWKEVEKGGDKDKPMPKQTFDELVEVCTTIWIASALHAANVF 721  
 Qy 736 GQPYGGVILNPTTSSRFMPVEGTAAYKELESNPEKAFRTICSELQALVSIIBILS 795  
 Db 722 GQPYGGVILNPTLSSRLPPEGTAAYDEVMVSSQKAYLATITPKQTLDLSVIELS 781  
 Qy 796 KHADEVILQPARSDWTSDKIALAPEKFGKUNFEVENRIMERKENVLNKRGPNLP 855  
 Db 782 RHASDEVILQRENPHWTSDSKALQAFQFGKLAIEAKLTNKNOPSLYHRYGVPQLP 841  
 Qy 856 YTLVFPSSNEGLTGRGIPNSISI 878  
 Db 842 YTLHPSSKEGLTFRGIPNSISI 864

RESULT 7  
 Lox3 PEa  
 ID Lox3 PEa STANDARD; PRT; 861 AA.  
 AC P09318;  
 DT 01-VAR-1989 (Rel. 10, Created)  
 DT 01-VAR-1989 (Rel. 10, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Seed lipoxigenase-3 (EC 1.13.11.12).  
 GN LOX1.3.  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OC NCBI\_TaxID=3888;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Brite;  
 RX MEDLINE=89025643; PubMed=3140791;  
 RA Baling P.M., Casey R.;  
 RT The complete amino acid sequence of a pea (Pisum sativum) seed  
 RL lipoxigenase predicted from a near full-length cDNA.";  
 RN Biochem. J. 253:915-918(1988).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Brite;  
 RA Casey R.;  
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF  
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND  
 CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO  
 CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING  
 CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.  
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-  
 CC hydroperoxyoctadeca-9,11-dienate.  
 CC -!- COFACTOR: Iron.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
 CC -!- SIMILARITY: Contains 1 PLAT domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL; X07807; CAA30666.1; -;  
 DR EMBL; X78581; CAA55319.1; -;  
 DR PIR; S01142; S01142.  
 DR HSSP; P09186; LLNH.  
 DR InterPro; IPR00907; Lipoxigenase.  
 DR InterPro; IPR001024; Lipoxigenase\_LH2.  
 DR InterPro; IPR008976; PLAT\_LH2.  
 DR Pfam; PF00305; lipoxigenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; P00087; LIPOXYGENASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
 DR PROSITE; PS00811; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS00951; PLAT; 1.  
 KW Oxidoreductase; Dioxigenase; Iron; Multigene family.  
 FT DOMAIN 41 166  
 FT METAL 522 522 IRON (BY SIMILARITY).  
 FT METAL 527 527 IRON (BY SIMILARITY).  
 FT METAL 713 713 IRON (BY SIMILARITY).  
 FT METAL 861 861 IRON (BY SIMILARITY).  
 SQ SEQUENCE 861 AA; 97628 MW; 442510278225D750 CRC64;  
 Query Match 57.7%; Score 2696.5; DB 1; Length 861;  
 Best Local Similarity 58.3%; Pred. No. 4.4e-176;  
 Matches 506; Conservative 145; Mismatches 184; Indels 33; Gaps 7;  
 QY 30 ILDRVSSLGNGIKGKIVLMRSNVLDFT-----EFHNLNDNTTELLGGVVS 76  
 DB 8 ILNR-----GHKIKGTIVLMRKXNVLDSLTVTGGVIGQGFILGSTVDNLTAFI LGRSVS 62  
 QY 77 FOLISATHTSNDGRGKGNKAYLEERWLSIPPLFAGESVQINFQWDFNFGFPGAFFIKN 136  
 DB 63 LQLISATKPDATGKGLGKATFLEGLISLFTLGLGQSAFKHFHDDMDGIPGAFYIKN 122  
 QY 137 GHTSEFFKSLTLDVPGVGRVHPCSNWVPSGYSKKDRIPFANHYVLPQTPNPLKRY 196  
 DB 123 FMQTEFFVSLTLDIPNHGSIYFVCSNWIYNAHKIKIDRIPFANQTYLPSETPAVLVY 182  
 QY 197 REELNWLRGDGTGRKEWDRIVDYVDNDIADPDVGDH--RPILGGITEYPPRRGRGTG 254  
 DB 183 REELNWLRGDGTGRKEWERIYDYVDNDLGNPSNGENHARPVLGGSETTYPPRRGRGTG 242  
 QY 255 RPRSRDRHNYEURLSPIMSLDIYVPKDNENFGLKMSDFGLYTLKALSIKIPGLQSI F-- 312  
 DB 243 RXPTRKDPNSES R-----SDYVYLRDEAFGLKSSDFLYGLKAVSQNVVPALESVF 297  
 QY 313 -DVTPNEFPNFKEVDNLPERGPIFPNAPKTTEDLTP-PLFKALVRNDGKFLKFPTE 370  
 DB 298 LNFPTNEFDSFDEVHGLYEGGKILPTN-----ILSQISPLVLKEIFRTDGTNTLYPPPK 353  
 QY 371 VVKDNKIGWSTDEEFAREMLAGNPILLIRLEAFPTSKLDPNVYGNQNSITTEHIIKHG 430  
 DB 354 VTQVSSGHWMTDEEFAREMLAGNVNVCCLQEFPPRSKLDQIYGDHTSKISKEHLRN 413  
 QY 431 LDGLTVDEAMKQNRLYIVDFHDALMPYTRMNATKTYATRTLLLLKDDGTLKPLVIEL 490  
 DB 414 LEGLATVEEAIGNKQLFLDLHDSIMPYLRRINSTKAYATRTILFLNNQNLKPLAIEL 473  
 QY 491 ALPHPGDGLGALSKLYRPAENGVOKSIWQLAKAVYVNDVGVYHQLISHWLHTHAVLPFP 550  
 DB 474 SLPHPGDDEHGA VSYVQPALEGVSSWLLAKAVYVNDSCYHQLVSHLWTHAVPEFF 533  
 QY 551 VIATHRQLSVLHPHKLVLPHYKDTMTFINASARQVLINANGLIETHYPSKYSMELSSIL 610  
 DB 534 VIATNRHLSCLHPYKLLVPHYRDTMNINSLARSLVNDGGIIEKTFIWLGRYSMEMSSKY 593  
 QY 611 YKDWTFPDQALPNMLKGLAVEDSSAPGLLELLINDYPAVDGLDIWAIAKTTWQDYCC 670  
 DB 594 YKNWVTEQALPADLIKRGNAIEDSSPCGVKLVVDYPIYAVDGLIWAIAKTTWQDYVS 653  
 QY 671 LYKDKDNAYQNDFELQSWNELREKHADKHEPMPKOTLSELIESCTTIWIASALH 730

Db 654 LYTSDEKLQDSLOAWKELVEVGHGDKQNEPWPQKQTRDLEIVCSIVITASALH 713  
 QY 731 AAVNGQYGYILNRPTRRRFMEVGTATYKELESNPKAFRLTICSELQALVSISI 790  
 Db 714 AAVNGQYSGYGLIILNRPTRRRFMEVGTATYKELESNPKAFRLTICSELQALVSISI 773  
 QY 791 TEILSKHASDEVYLGORASIDWTSKIALEAFKFGKULFEVENRIMERKEVNLKRSRG 850  
 Db 774 TEILSKHASDEVYLGORASIDWTSKIALEAFKFGKULFEVENRIMERKEVNLKRSRG 833  
 QY 851 PVNPTLLVPSSNEGLTGRGPNISISI 878  
 Db 834 PVNPTLLVPSSNEGLTGRGPNISISI 861

RESULT 8  
 LOX2 SOYBN STANDARD; PRT; 865 AA.  
 ID LOX2 SOYBN STANDARD; PRT; 865 AA.  
 AC P09439;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Seed lipoxigenase-2 (EC 1.13.11.12) (L-2).  
 GN LOX1.2 OR LOX2.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 CX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86198254; PubMed=2834391;  
 RA Shibata D., Steczko J., Dixon J.E., Andrews P.C., Hermodson M.,  
 RA Axelrod B.;  
 RT "Primary structure of soybean lipoxigenase L-2";  
 RL J. Biol. Chem. 263:6816-6821(1988).  
 RN [2]  
 RP SEQUENCE OF 231-865 FROM N.A.  
 RA Start W.G., Ma Y., Polacco J.C., Hildebrand D.F., Freyer G.A.,  
 RA Altschuler M.;  
 RT "Two soybean seed lipoxigenase nulls accumulate reduced levels of  
 lipoxigenase transcripts";  
 RL Plant Mol. Biol. 7:11-23(1986).  
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF  
 DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND  
 DEVELOPMENT, PEST RESISTANCE, AND SENSATION OF RESPONSES TO  
 WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING  
 A CIS, CIS-1,4-PENTADIENE STRUCTURE.  
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13E)-13-  
 hydroperoxyoctadeca-9,11-dienoate.  
 CC -!- COFACTOR: Iron, one atom tightly bound per molecule.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,  
 L-1, L-2, L-3A, AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT  
 ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.  
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
 CC -!- SIMILARITY: Contains 1 Pfam domain.  
 CC -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN AT POSITIONS 691  
 TO 865 DUE TO A FRAMESHIFT.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; J03211; AAA33987.1; -  
 DR PIR; A28161; DASYL1.  
 DR HSSP; P08170; 2SBL.  
 DR InterPro; IPR000907; Lipoxigenase.

DR InterPro; IPR001024; Lipoxigenase\_LH2.  
 DR InterPro; IPR008976; PLAT LH2.  
 DR Pfam; PF00305; lipoxigenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PRO0087; LIPOXYGENASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS00095; PLAT; 1.  
 KW Oxidoreductase; Dioxigenase; Iron; Multigene family.  
 FT METAL 50 175  
 FT METAL 527 527 IRON (BY SIMILARITY).  
 FT METAL 532 532 IRON (BY SIMILARITY).  
 FT METAL 718 718 IRON (BY SIMILARITY).  
 FT METAL 865 865 IRON (BY SIMILARITY).  
 FT CONFLICT 263 264 KP -> NL (IN REF. 2).  
 FT CONFLICT 313 313 D -> Y (IN REF. 2).  
 FT CONFLICT 400 400 L -> P (IN REF. 2).  
 FT CONFLICT 428 428 L -> H (IN REF. 2).  
 FT CONFLICT 486 486 D -> G (IN REF. 2).  
 FT CONFLICT 502 502 V -> G (IN REF. 2).  
 FT CONFLICT 534 534 V -> L (IN REF. 2).  
 SQ SEQUENCE 865 AA; 97145 MW; 74CBD32E3E4A0C85 CRC64;  
 Query Match 57.5%; Score 2690; DB 1; Length 865;  
 Best Local Similarity 58.4%; Pred. No. 1.2e-175;  
 Matches 513; Conservative 127; Mismatches 194; Indels 44; Gaps 8;  
 QY 23 VINAGNILDVRSSLGNGKIKGVILMRSNVLDPTEFH-----SNLL 64  
 Db 10 ILNRG-----GGHKIKGTIVLMRKNVLDNFNSVADLTGKNGVGLTGTGLNVGVSTL 59  
 QY 65 DNFTELLGGVSPOLISATHTSNDRGKVGKAYLERWLTSPPLFAGESVQINFWDE 124  
 Db 60 DNLTAFLGRSVALQLISATKPLANGKRGVKGTFTLEGIIVSPTLGAGESAFNIOFWD 119  
 QY 125 NFGFGGAFFIKNGHTSEFFELKSLTLDVDPGYGRVDFDCNSWYVPGRYKKDRIFFANHY 184  
 Db 120 SMGIPGAFYIKVMQVEFYLYKSLTLEDVFNQGTIRFCVNSWYVNTKLYKSVIRFANHY 179  
 QY 185 LPSOTNPLRKRYREBELNLRGDTGGERKEWRIYDYVDYNDIADDDVGDH--RILG 242  
 Db 180 VPESETPAALVGYREBELKNLRGDTGGERKEHRIYDYVDYNDLGNPDHGFARFILGS 239  
 QY 243 TEYPYPRGRGTRPRSRDRHYESRLSPIMSDIYVVDENFGLKMSDFLYTKALSI 302  
 Db 240 SHYPYPRGRGTRGYPTKQNSEK-----PGEVYVPRDENFGLKSSDFLAYGKLSQ 293  
 QY 303 SIKPGHQSIQFDV--TPNEFDNPEVDNLPFERGFIPFNKFTLTEDLTPPLFKALVRNDG 360  
 Db 294 YVLPAPFESVFDLNFTEPNEFDSPQDVRDLHEGGIKLPTEVISTI---MPLPVVKELFR 350  
 QY 361 EKFLKPTPEVVKDNKIGWSTDEFAREMLAGNPULLRLEAFPTSKLDNPNVGNQS 420  
 Db 351 EQVLKPPPHVIVQVSKSAMWTDDEFAREMVAGVNCVIRGLQEPFKSNLDPTIIGEQTS 410  
 QY 421 TITEEHKGLDGLTVDEAMQNRLIYVDFHDALMPYLTRMNATSTKYATRTLLKDD 480  
 Db 411 KITADAL--DLGGYTVDEALSGRLFLMDYHDFVFPYRRINQTYAKAYATRTILFLRN 468  
 QY 481 GTLKPLVIELALPHPGDQDGLGKILYPPAENGVOKSIWOLAKAYVNDVYHOLISHW 540  
 Db 469 GTLKPLVIELALPHPGDQDGLGKILYPPAENGVOKSIWOLAKAYVNDVYHOLISHW 528  
 QY 541 LHTHAVLEPFVLTATHRQLSVLHPHKLIVPHYKDMFMINASARQVLINANGLIETHVPS 600  
 Db 529 LANTHAVIEFFIATNHLNLSALHPHYKLLTPHYRDTMNLARQSLINADGIIKSFUPS 588  
 QY 601 KYSMELSSILYKDWTPPDQALPNMLKRGVLAEDSSAPHLRLLINDPFAVDGLDINSA 660  
 Db 589 KHSVEMSSAVYKXWVFTDQALPADLTKRGVAIKPSAPHLRLIEDYFAYVDGLGELWAA 648  
 QY 661 IKTWQDYCCLYVKDDNAVQNDPFLQSWWNLREKGHADKKHEPWWPKMQLSELIESCT 720

```

Db 649 IKTWQEVSLYYARDVDDKSELOQWKAWEKGGHGLKDKPWWKFLQIEBLVICT 708
QY 721 TIWIASALHAANFGQYGYILNRPTTERRFMPEVGTAYEYKELESNPKEAFLRTICS 780
Db 709 IITWIASALHAANFGQYGYILNRPTTERRFMPEVGTAYEYKELESNPKEAFLRTICS 768
QY 781 ELQALVSIITILSKHASDEVYLGORASIDWTSKIALEAFKFGKLEFVENRIMERN 840
Db 769 KFTUVDUSVIBILSRHASDEVYLGORNDPHWTSKALQAPQKFGKLEBIEKLARKN 828
QY 841 KEWNLKRSQPNVLYTYLLVPSNBNGLTCRGIPNSISI 878
Db 829 NDOSLNRLGPVQLPYTYLLHPNS-EGLTGCGIPNSISI 865

RESULT 9
LOXX SOYBN
ID LOXX SOYBN STANDARD; PRT; 864 AA.
AC P24095;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seed lipoxigenase (EC 1.13.11.12).
GN LOX1.4 OR SC514.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxId=3847;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Williams 82; TISSUE=Radicle;
RC Park T., Holland M.A., Laskey J.G., Polacco J.C.;
RA Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: GERMINATED COTYLEDONS.
CC -!- INDUCTION: By jasmonate.
CC -!- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
CC L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
CC ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56139; CAA39604.1; -.
CC EMBL; U04526; AAA03728.1; -.
CC PIR; S13381; S13381.
CC HSP; P08170; 2SBL.

```

```

DR InterPro: IPR000907; Lipoxigenase.
DR InterPro: IPR001024; Lipoxigenase_LH2.
DR InterPro: IPR008976; PLAT_LH2.
DR Pfam: PF00305; lipoxigenase; 1.
DR PRINTS; PF01477; PLAT; 1.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Oxidoreductase; Dioxigenase; Iron; Multigene family.
FT DOMAIN 44 171 PLAT.
FT METAL 525 525 IRON (BY SIMILARITY).
FT METAL 530 530 IRON (BY SIMILARITY).
FT METAL 716 716 IRON (BY SIMILARITY).
FT METAL 864 864 IRON (BY SIMILARITY).
FT CONFLICT 233 233 S -> C (IN REF. 2).
FT CONFLICT 240 240 R -> L (IN REF. 2).
FT CONFLICT 604 604 D -> H (IN REF. 2).
FT CONFLICT 695 695 M -> K (IN REF. 2).
SQ SEQUENCE 864 AA; 96816 MW; 66F31PB1FA5F3B60 CRC64;

Query Match 56.6%; Score 2644.5; DB 1; Length 864;
Best Local Similarity 58.1%; Pred. No. 1.6e-172; Indels 37; Gaps 7;
Matches 504; Conservative 125; Mismatches 201;

QY 39 GNKIGKGVILMRSNVLDTEFHS-----NLLDNFTELGGGVS 76
Db 8 GQKIGTGVLMKPNVLDNFNAITSIGKGVVDITATGILQGVSLVGGVIDTATSLGRNIS 67
QY 77 FOLISATHTSNDGRGVKNKAYLERWLTISPLPAGESVFOINFOWDENFGFGAFFTKN 136
Db 68 MQLISATQDGGNGKGVKGVLEKHLPTLPFLGARQDAFSIFFEWDASFGIPGAFYIKN 127
QY 137 GHTSPFFKSLTLDVDPVGRVHFDNCNVWVPSGRYKDKRIFFAHNVLPSTQNPRLKY 196
Db 128 FMTDFEFLVSKLEIDPNHGTFIEVCNSVWYFRSYKKNRIFVNDTVLPSATPAPLLKY 187
QY 197 REELNWRGDTGERKWDRIYDVNDIADPVGDHRPILGTTGTPYPRRGTORP 256
Db 188 RKEELEVLGDTGKGRKDFRIYDVNDVNDLGNPDGDPRIPLGSSIVPYPRRVRTGORE 247
QY 257 RRRDHNVESRLSPIMSLDIYVVKDENFCHLQMSDFLGVTLKALISISIKPLQS-IFD-- 313
Db 248 RRTDPNEX-----PGEVYVPRDENFGHLKSSDFLYGKLSHVDVLPFKSAIFQLR 301
QY 314 VTPNEFDNPKVDNLFERGFPIPFNAFKTLTDLTP-PLFKALVNDGKELKFPPTPEV 372
Db 302 VTSSEFSESPEDVRSLYEGGKILPTD-----ILSQISPLPALKEIFRTDGENVLQFPPHVA 357
QY 373 KDKTCWSTDEEFAREMLAGNPILIRLEAPPTSKLDPNVYGNQNSTITEEHKGLD 432
Db 358 KVSXGMMTDEEFAREVIAGVNPVIRLQEPFKSTLDPLTLYGDTSTIINEKEINWG 417
QY 433 GLTVDEAMKQNRLYIVDFHDMALPILTRMNTST-KTYATRTLLLLKDDGTLPKLVIELA 491
Db 418 GVTVEALSTQRLFDLYQDAFIPVLTIRNSLPTAKAVATRIILFKDDGTLPKLAELS 477
QY 492 LPHQGDQGLGALSKLYFFAENGQVKSINQLAKAVYVNDGVHQLISHWLTHAVLEP 551
Db 478 KFHPPGDNLGPESIVVLVATGEGVSTIWLAKAHVINDSVGHQVLVSHWLANTHAWNSPFA 537
QY 552 IATHPQLSVLHPHILKLLVPHYKDTMFINASARQVLINANGLTITHTYPSKYSMELSSILY 611
Db 538 IATNRLSVLHPHILKLLVPHYEDTININGLAQSLINADGIIKESFLPGKYSIEMSSSV 597
QY 612 KDWTFPDQALPNMLMKRGLAVEDSSAPHLRLINDYFPAVDGLDINSATITWYDYL 671
Db 598 KKWVTDQALPADLVKRGILAIEDPSAPHLRLVIEDYFPAVDGLDINSATITWYDYL 657
QY 672 YVKDNDVAVDPELOSWMNELREKGHADKCHPEWPKMQTLSELTSTETIIWIASALHA 731
Db 658 YFPTDAAVQDDTELOAWKKEAVEKGGHGLKDKPWWKFLQIEBLVICT 717

```

QY 732 AVNFGQYVGGVILNRPPTSRPFMEVGTABYKELESNPEKAFLEATICSLEQALVSI 791  
 Db 718 AVNFGQYVGGVILNRPPTSRPFMEVGTABYKELESNPEKAFLEATICSLEQALVSI 777  
 QY 792 EILSHASDEVYLGORASIDWTSKIALEAEKFGKLNLFVENRIMERNKEVNLKNSGP 851  
 Db 778 EILSHASDEVYLGORASIDWTSKIALEAEKFGKLNLFVENRIMERNKEVNLKNSGP 837  
 QY 852 VNLPTVLLVPSNEGLTGRTGIPNSISI 878  
 Db 838 VOLPPTVLLVPSNEGLTGRTGIPNSISI 864

RESULT 10  
 LOXA PHAVU  
 ID LOXA PHAVU STANDARD; PRT; 862 AA.  
 AC P27480;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Lipoxigenase 1 (BC 1.13.11.12).  
 GN LOXA OR LOX1  
 OS Phaseolus vulgaris (Kidney bean) (French bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
 OX NCBI\_TaxID=3885;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=sv. Red Mexican; TISSUE=Leaf;  
 RX MEDLINE=94171713; PubMed=8130796;  
 RA Eiben H.G.; Slusarenko A.J.;  
 RT "Complex spatial and temporal expression of lipoxigenase genes during  
 Phaseolus vulgaris (L.) development.";  
 RL Plant J. 5:123-135 (1994).  
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF  
 DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND  
 DEVELOPMENT, PEST RESISTANCE, AND SENSITIVE OR RESPONSES TO  
 WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING  
 A CIS, CIS-1,4-PENTADIENE STRUCTURE.  
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-  
 hydroperoxyoctadeca-9,11-dienoate.  
 CC -!- COFACTOR: Iron, one atom tightly bound per molecule.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
 CC -!- SIMILARITY: Contains 1 PLAT domain.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X63525; CA445088.1; -.  
 DR PIR; S22153; S22153.  
 DR HSGP; P08170; 2SBL.  
 DR InterPro; IPR000907; Lipoxigenase.  
 DR InterPro; IPR001024; Lipoxigenase\_LH2.  
 DR InterPro; IPR008976; PLAT\_LH2.  
 DR Pfam; PF00305; lipoxigenase\_1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXYGENASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS00095; PLAT; 1.  
 KW Oxidoreductase; Dioxigenase; Iron; Multigene family.  
 FT DOMAIN 44 171 PLAT.  
 FT METAL 522 522 IRON (BY SIMILARITY).

FT METAL 527 527 IRON (BY SIMILARITY).  
 FT METAL 713 713 IRON (BY SIMILARITY).  
 FT METAL 862 862 IRON (BY SIMILARITY).  
 SQ SEQUENCE 862 AA; 97154 MW; 24566D1CEE3C191E CRC64;  
 Query Match 55.5%; Score 2596; DB 1; Length 862;  
 Best Local Similarity 56.7%; Pred. No. 3.2e-169; Indels 42; Gaps 9;  
 Matches 496; Conservative 142; Mismatches 195;  
 QY 30 ILDRVSSLOGNKIKGVILMNSVLDTFEFHS-----NLLDNF 67  
 Db 4 ILNR-----GHKIKGTWLMTKNVDFNEFVSTRGGIVGAAGGLFGAATDIVGGIVDCA 58  
 QY 68 TELGGGVFOLISATHTSNDGRKGVKAYLERWLTISIPPLFAGESVFOINFDWNG 127  
 Db 59 TAIFSRNIAIQLISATKTDLGLNGKVGKQTFLEKHLPSLNLGDRQDAFNVFVFEWDENFG 118  
 QY 128 FPGAFFIKNGHTSEFFELKSLTLDVPGYGRVHFDGNSWVYPSGRYKDKRIFFANHVLP 187  
 Db 119 IPEAFYIKFMQSEFFLVSLTLEDIPNHTGIHFVCSWYVNAKSKYKDRIFANKTYL 178  
 QY 188 QTENPLKRYREBELMNLRGDGTGERKEDRIYDYVDYNDIADPDVGDH--RPILGTTY 245  
 Db 179 ETPASLVKRYKELENLRGDTGERKEYDRIYDYVYNDLGNPKNKLARTTLOGSSDF 238  
 QY 246 PYPRRGRTGKPRRRDHNYESRLSPIMSLDIYVPDENFGHLKMSDFGLGYTLKALISITK 305  
 Db 239 PYPRRGRTGKTRDKPCE-----IPTSDTTPRDENFGHLKSGDFLYAIKSLTONVL 293  
 QY 306 PGLQSFIDVTPNEFDNFKVDNLFERGFPIPPNAPFKLTEDTLPPLKALVRNDGKFLK 365  
 Db 294 PTFQKAFGN-NEFDTFEDVGRGLFEGGLYLPDVTISKIS--PIPVLEILRTDGEQVLK 349  
 QY 366 FPPPEVVDKNKIGWSTDEFEAREMAGNPLIRLEAPPTSKLDPNVYQNSNTIIEE 425  
 Db 350 FPPPHVIRVTKSAMTDEEFREMGELAGVNPCLIQRLQEPFPPSKLDVTVYGDSTMTKE 409  
 QY 426 HKHGDGLTVDKAMQNRLYIVDFHDALMPYLTMNATST-KTYATRTLLLKDDGLTK 484  
 Db 410 HLEINLGLTVEALHGNRLFILDHDAFIPYLERINDLPYAKVATRTILFKDNTILK 469  
 QY 485 PLVIELALPHQDQGLGALSILYPAENGVOQKSIQOLKAYVYVDVGVHQLISHWLTH 544  
 Db 470 PLAIELSLPNPGK--GANSRVILPADGGAESTIWLAKAYVYVNDSCYHQLMSHLNTH 527  
 QY 545 AVLEPEVIATHRQLSVLHPHKLPHYKDTMFINASQVLINANGLIETTHYPSKYSM 604  
 Db 528 AVNEPVIATNRHLSVLHPHKLPHYEDTWNINARQSLINAGGVIERSFLEGEFV 587  
 QY 605 ELSSILYKDWTPDQALPNLMKRGVAVEDSSAPHLRLINDYPAVDGLDIWSAIKTW 664  
 Db 588 EMSSAVYKSWVFTDQALPADLIRGMVAVEDPSSPYGLRVVSDYPAVDGLDIWDTIQTW 647  
 QY 665 VODYCLLYKDDNAVQNDPELOSWNELREKHAQKHEPWPMPKQTLSELIESCTTIW 724  
 Db 648 VKDYVSLYPTNDVAKKOTELQAWKEAVEKGHGLKDKPMPKLTQDILLTCSIIW 707  
 QY 725 IASALHAAVNFQYVGGVILNRPPTSRPFMEVGTABYKELESNPEKAFLEATICSLEQ 784  
 Db 708 IASALHAAVNFQYVGGVILNRPPTSRPFMEVGTABYKELESNPEKAFLEATICSLEQ 767  
 QY 785 LVYSISIIETLSKASDEVYLGORASIDWTSKIALEAEKFGKLNLFVENRIMERNKEV 844  
 Db 768 IVDLSVIELSRHASDEVYLGORASIDWTSKIALEAEKFGKLNLFVENRIMERNKEV 827  
 QY 845 LKNRSGPVNLPYLLVPS--SNEGLTGRTGIPNSISI 878  
 Db 828 LKNRSGPVNLPYLLVPS--SNEGLTGRTGIPNSISI 862

RESULT 11  
 LOX4 SOYBN  
 ID LOX4 SOYBN STANDARD; PRT; 853 AA.



AC P38417;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Lipoxigenase-4 (EC 1.13.11.12) (L-4) (VSP94).  
 GN LOX1.5 OR LOX4.  
 OS Glycine max (soybean).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 CC eudicots I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 CC NCBI TaxID=3847;  
 RN [1]\_TaxID=3847;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Enrei;  
 RA Kato T., Shirano Y., Iwamoto H., Shibata D.;  
 RT "Soybean lipoxigenase L-4, a major component of the 94-kilodalton  
 RT storage protein in vegetative tissues: expression and accumulation in  
 RT leaves induced by pod removal and by methyl jasmonate.";  
 RL Plant Cell Physiol. 34:1063-1072(1993).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 CC TISSUE=Cotyledon;  
 RA Kato T., Ohta H., Tanaka K., Shibata D.;  
 RT "Appearance of new lipoxigenases in soybean cotyledons after  
 RT germination and evidence for expression of a major new lipoxigenase  
 RT gene.";  
 RL Plant Physiol. 98:324-330(1992).  
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF  
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND  
 CC DEVELOPMENT, PEST RESISTANCE, AND SENSITIVE OR RESPONSES TO  
 CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING  
 CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.  
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-  
 CC hydroperoxyoctadeca-9,11-dienoate.  
 CC -!- COFACTOR: Iron, one atom tightly bound per molecule.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- TISSUE SPECIFICITY: FOUND IN MATURING AND DEVELOPING SEEDS. IN  
 CC YOUNG SEEDLINGS IT IS FOUND IN COTYLEDONS, HYPOCOTYLS, ROOTS AND  
 CC PRIMARY LEAVES.  
 CC -!- DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED. EXPRESSION IS HIGH  
 CC 3 TO 5 DAYS AFTER GERMINATION AND RETURNS TO BASAL LEVEL BY DAY 9.  
 CC -!- INDUCTION: BY POD REMOVAL AND METHYL JASMONATE.  
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
 CC -!- SIMILARITY: Contains 1 PLAT domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announcement/)  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: D13999; BAB03101.1; --  
 CC EIR; T07662; T07662.  
 CC HSP; P09186; ILNH.  
 CC InterPro: IPR000907; Lipoxigenase.  
 CC InterPro: IPR01024; Lipoxigenase\_LH2.  
 CC InterPro: IPR008976; PLAT LH2.  
 CC Pfam: PF00305; Lipoxigenase; 1.  
 CC Pfam: PF01477; PLAT; 1.  
 CC PRINTS: PR00087; LIPOXYGENASE.  
 CC SMART; SM00308; LH2; 1.  
 CC PROSITE; PS00711; LIPOXYGENASE\_1; FALSE\_NEG.  
 CC PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 CC PROSITE; PS00095; PLAT; 1.  
 CC Oxidoreductase; Dioxxygenase; Iron; Multigene family.  
 CC DOMAIN 34 159 PLAT  
 FT METAL 513 513 IRON (BY SIMILARITY).  
 FT METAL 518 518 IRON (BY SIMILARITY).  
 FT METAL 704 704 IRON (BY SIMILARITY).  
 FT METAL 853 853 IRON (BY SIMILARITY).

SQ SEQUENCE 853 AA; 96534 MW; 533175EE1CFB34FC CRC64;

Query Match 55.4%; Score 2591; DB 1; Length 853;  
 Best Local Similarity 57.4%; Pred. No. 6.9e-169;  
 Matches 492; Conservative 133; Mismatches 204; Indels 28; Gaps 10;

QY 39 GNKIKGKILMESNVLDTFEHS--NLADNFTLLGGV-----SFLISATHTS 86  
 DB 8 GQKIKGTVMVQKNVLDINSITSGVIGQGLGFGSAVDALTFAATKISQLISAT-KA 66  
 QY 87 NDSRGKVGKAYLERWLTSIPDLFAGESVFQINFQWENFPGPFAFFKNGHTSEFFLKS 146  
 DB 67 DGGKKGKIGKSTNLGKIT-LPTLGAGEQAYDNFWDSDFGIPGAFYIKNFQNEFYLKS 125  
 QY 147 LTLDDVPVGRVHFDCNSWVPISGKDYKDRIFPANHVLPSQTPNPLKRYEELNLNRG 206  
 DB 126 LILEDPINHTTHFCVNSWVNSKNYKTRIFPANNYLPSETPAPLKYEEELKNVRG 185  
 QY 207 DGTGERKEWDRIYDYVDVNDIADPDVGDH--RPILGGTTEYPYPRRGRTGRPRRDHNY 264  
 DB 186 DGTGERKEWDRIYDYVDVNDLGNPDSDGKYARFVLGSSA-LPYPRERTGRKTRKDPNS 244  
 QY 265 ESRLSPIMSLDIYVPKDNFGLKMSDFGLYTLKALSISIKFGLQSIFD--VTPNEPQNF 322  
 DB 245 EK-----PSDFVYLPRDEAFGLKSSDFLAYIKSVSQDVLFLVDAFDGNILSLEPQNF 299  
 QY 323 KEVDNLFERGFPPIPNFAKTLTDLTPPLFKALVNDGKFKLFTPTPEVVKDKIKGSTD 382  
 DB 300 AEVHKLYEGCVTLPTN---FLSKIAPIVKEIFATDGEQFLKYPKPKVMQVDKSAWTD 356  
 QY 383 EFAREMLAGNPLIRLEAPPTSKLDPNVGNQNSTITEEHKHLGDLGTLVDEAMKQ 442  
 DB 357 EBFARETIAGLNPNWIKIEEPFLSKLDTOAGDHTCIIAKEHLEPNLGLSLTVEQAION 416  
 QY 443 NRIYIVDHDALMEVYLTRMNTSTKYATRTLLKDDGTLKPLVIELALHPQDDQLGA 502  
 DB 417 KGLFLDHDHYLIPIYLRKINANTTYATRTIFFLKDDGTLTPLAIELSKPHQEEYGP 476  
 QY 503 ISKLYPPAENGQKSIWQLAKAYTVNDVGVHQLISHMLHVALEPFIATHRLSVLH 562  
 DB 477 VSEVYVPASEGVEAVIWLAKAYVVNDACYHQIISHWLSTHAIVEPFIATNRLSVVH 536  
 QY 563 PIHKLIVPHYKDTMFINASARQVLINAGLIETHYPSKYSMELSSILYKOWTFPDQALP 622  
 DB 537 PIYKLLFPHYRDTMINSARKALVNDAGIIEKTFWGRYSMEASAVYKOWTFDQALP 596  
 QY 623 NNLMRKGLAVEDSSAPHGLRLINDYPAVDGLDIWSAIKTWQDYCYCLYYKDDNAVQND 682  
 DB 597 NDLVKEGVAVKPSAPHGVRLIEDYPAVDGLDIWSAIAKSWVQSVYKSDDELOKD 656  
 QY 683 FELQSWNELREKGHADKKEHPWPKMQLTSLIESCTTIWIASHALHAANVFGOPYGG 742  
 DB 657 PELQAWKVELVEVGHGDLKKEWQKQVTRSELVEASAILIWIASHALHAANVFGOPYGG 716  
 QY 743 YILNRPTTSRRFMPEVGTAYEYKELESNPEKALRTICSELOALVSIISIIILSKASDEV 802  
 DB 717 LILNRPTTSRRFMPEKSPEDYDALAKNPEKFLKITGKTKETLIDLTVIELLSRSHASDEF 776  
 QY 803 YLGQASID-WTSDKIALAEAFKPGKNUFEVNRIMERNKENVNKNRSGFVNLPYTLVLP 861  
 DB 777 YLGQDGGDYWTSDAGPLEAFKFRFGKLEIEKLEIEKLEIEKLEIEKLEIEKLEIEKLEIE 836  
 QY 862 SSNEGTLTGEGIPNSISI 878  
 DB 837 SSEEGLTFRGIPNSISI 853

RESULT 12

LOX1 SOYBN  
 ID LOX1 SOYBN STANDARD; PRT; 839 AA.  
 AC P08170;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Seed lipoxygenase-1 (EC 1.13.11.12) (L-1).  
 GN LOX1.1 OR LOX1.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID:3847;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=87280024; PubMed=3112136;  
 RA Shibata D., Steczko J., Dixon J.E., Hermodson M., Yazdanparast R.,  
 RA Axelrod B.;  
 RT "Primary structure of soybean lipoxygenase-1";  
 RL J. Biol. Chem. 262:10080-10085 (1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Bonminor; TISSUE=Cotyledon;  
 RA Fukazawa C., Masayoshi M., Chikafusa F.;  
 RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 426-752 FROM N.A.  
 RA Start W.G., Ma Y., Polacco J.C., Hildebrand D.F., Freyer G.A.,  
 RA Altschuler M.;  
 RT "Two soybean seed lipoxygenase nulls accumulate reduced levels of  
 RT lipoxygenase transcripts";  
 RL Plant Mol. Biol. 7:11-23 (1986).  
 RN [4]  
 RP MUTAGENESIS OF SOME HISTIDINE RESIDUES, AND REVISIONS TO 479-482.  
 RX MEDLINE=92232702; PubMed=1567851;  
 RA Steczko J., Donoho G.P., Clemens J.C., Dixon J.E., Axelrod B.;  
 RT "Conserved histidine residues in soybean lipoxygenase: functional  
 RT consequences of their replacement";  
 RL Biochemistry 31:4053-4057 (1992).  
 RN [5]  
 RP MUTAGENESIS OF SOME HISTIDINE RESIDUES.  
 RX MEDLINE=92360013; PubMed=1497657;  
 RA Steczko J., Axelrod B.;  
 RT "Identification of the iron-binding histidine residues in soybean  
 RT lipoxygenase L-1";  
 RL Biochem. Biophys. Res. Commun. 186:686-689 (1992).  
 RN [6]  
 RP ACTIVE SITE, AND IRON LIGANDS.  
 RX MEDLINE=93298753; PubMed=8518276;  
 RA Minor W., Steczko J., Bolin J.T., Otwinowski Z., Axelrod B.;  
 RT "Crystallographic determination of the active site iron and its  
 RT ligands in soybean lipoxygenase L-1";  
 RL Biochemistry 32:6320-6323 (1993).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RX MEDLINE=93276267; PubMed=8502991;  
 RA Boyington J.C., Gaffney B.J., Amzel L.M.;  
 RT "The three-dimensional structure of an arachidonic acid  
 RT 15-lipoxygenase";  
 RL Science 260:1482-1486 (1993).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).  
 RX MEDLINE=96345062; PubMed=8718858;  
 RA Minor W., Steczko J., Stec B., Otwinowski Z., Bolin J.T., Walter R.,  
 RA Axelrod B.;  
 RT "Crystal structure of soybean lipoxygenase L-1 at 1.4-A resolution";  
 RL Biochemistry 35:10687-10701 (1996).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).  
 RX MEDLINE=21305677; PubMed=11412104;  
 RA Tomchick D.R., Phan P., Cymborowski M., Minor W., Holman T.R.;  
 RT "Structural and functional characterization of second-coordination  
 RT sphere mutants of soybean lipoxygenase-1";  
 RL Biochemistry 40:7509-7517 (2001).  
 RN [10]  
 RP FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF  
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND  
 CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO  
 CC WOUNDING. WITH LINOLEATE AS SUBSTRATE, L-1 SHOWS A PREFERENCE FOR

CC CARBON 13 AS THE SITE FOR HYDROPEROXIDATION (IN CONTRAST TO L-2  
 CC AND L-3 WHICH UTILIZE EITHER CARBON 9 OR 13).  
 CC -1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-  
 CC hydroperoxyoctadeca-9,11-dienoate.  
 CC -1- COFACTOR: Iron, one atom tightly bound per molecule.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- INDUCTION: THE HYDROPEROXIDE PRODUCT SERVES TO ACTIVATE THE  
 CC RESTING ENZYME. THE ACTIVATION IS ACCOMPANIED BY THE OXIDATION  
 CC OF FE(2+)-ENTADIENE STRUCTURE. L-1 PREFERENCES ANIONIC SUBSTRATE.  
 CC -1- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,  
 CC L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT  
 CC ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.  
 CC -1- SIMILARITY: Belongs to the lipoxygenase family.  
 CC -1- SIMILARITY: Contains 1 PLAT domain.  
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN AT POSITIONS 663  
 CC TO 697 DUE TO A FRAMESHIFT.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; J02795; AAA33986.1; -  
 CC EMBL; X67304; CAA47717.1; ALT\_FRAME.  
 CC PIR; S25064; DASYL2.  
 CC PDB; 1F8N; 04-JUL-01.  
 CC PDB; 1FGN; 24-OCT-01.  
 CC PDB; 1FGO; 04-JUL-01.  
 CC PDB; 1FGQ; 04-JUL-01.  
 CC PDB; 1FGR; 18-JUL-01.  
 CC PDB; 1FGT; 04-JUL-01.  
 CC PDB; 1YGE; 23-JUL-97.  
 CC PDB; 2SBL; 27-FEB-95.  
 CC InterPro; IPR000907; Lipoxygenase.  
 CC InterPro; IPR001024; Lipoxygenase\_LH2.  
 CC InterPro; IPR008976; PLAT\_LH2.  
 CC Pfam; PF00305; lipoxygenase; 1.  
 CC Pfam; PF01477; PLAT; 1.  
 CC PRINTS; PR00087; LIPOXYGENASE.  
 CC SMART; SM00308; LH2; 1.  
 CC PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
 CC PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 CC PROSITE; PS50095; PLAT; 1.  
 CC Oxidoreductase; Dioxxygenase; Iron; Multigene family; 3D-structure.  
 KW DOMAIN 16 145  
 FT METAL 499 499 IRON.  
 FT METAL 504 504 IRON.  
 FT METAL 690 690 IRON.  
 FT METAL 839 839 IRON.  
 FT MUTAGEN 494 494 H->Q: 37% OF WILD-TYPE ACTIVITY.  
 FT MUTAGEN 494 494 H->S: 8% OF WILD-TYPE ACTIVITY.  
 FT MUTAGEN 499 499 H->Q: INACTIVE.  
 FT MUTAGEN 504 504 H->Q: INACTIVE.  
 FT MUTAGEN 517 517 H->Q: 33% OF WILD-TYPE ACTIVITY.  
 FT MUTAGEN 522 522 H->Q: 1% OF WILD-TYPE ACTIVITY.  
 FT MUTAGEN 531 531 H->Q: 20% OF WILD-TYPE ACTIVITY.  
 FT MUTAGEN 690 690 H->Q: INACTIVE.  
 FT CONFLICT 426 427 AK -> RN (IN REF. 3).  
 FT CONFLICT 558 560 LPS -> AL (IN REF. 3).  
 FT CONFLICT 572 574 KNW -> EL (IN REF. 3).  
 FT CONFLICT 641 641 N -> P (IN REF. 3).  
 FT CONFLICT 741 748 KLPTLISL -> SCRLSLAV (IN REF. 3).  
 FT STRAND 7 16  
 FT HELIX 17 19  
 FT TURN 20 20  
 FT TURN 24 26  
 FT HELIX 32 35  
 FT TURN 37 38  
 FT STRAND 40 50

FT	TURN	52	53
FT	STRAND	56	58
FT	STRAND	62	63
FT	STRAND	66	68
FT	TURN	76	77
FT	STRAND	79	86
FT	HELIX	89	91
FT	STRAND	94	101
FT	STRAND	107	114
FT	TURN	117	120
FT	STRAND	123	131
FT	STRAND	133	133
FT	HELIX	134	136
FT	STRAND	141	144
FT	HELIX	151	153
FT	HELIX	156	158
FT	HELIX	159	170
FT	TURN	179	180
FT	STRAND	186	187
FT	STRAND	189	189
FT	TURN	195	197
FT	HELIX	199	201
FT	STRAND	206	206
FT	STRAND	217	218
FT	STRAND	224	224
FT	TURN	229	230
FT	STRAND	232	232
FT	HELIX	242	244
FT	HELIX	251	253
FT	HELIX	255	257
FT	HELIX	258	264
FT	TURN	265	265
FT	HELIX	266	275
FT	TURN	276	277
FT	HELIX	286	290
FT	HELIX	291	293
FT	TURN	294	295
FT	STRAND	297	298
FT	HELIX	301	307
FT	TURN	308	309
FT	TURN	311	312
FT	HELIX	313	316
FT	STRAND	318	319
FT	STRAND	324	326
FT	HELIX	331	333
FT	HELIX	339	341
FT	HELIX	343	352
FT	TURN	356	357
FT	STRAND	360	361
FT	HELIX	373	376

Query Match 55.2%; Score 2582.5; DB 1; Length 839;  
Best Local Similarity 58.7%; Pred. No. 2.6e-168;  
Matches 497; Conservative 124; Mismatches 208; Indels 17; Gaps 8;

QY	39	GKIKGKVILMESNVLDFTFESHNLNFTTELLGGGVSPQLISATHTSNDSRGKVGNKAY	98
DB	5	GHKIKGTVVVLMPPKNELEVP-DGSAVDNLNAFLGRSVLSQLISATXADAHGKGKVKGDTP	63
QY	99	LERWLTSIPPLPAGESVFQINFOWDENFGFPFGAFFINQNGHTEFFLKSLTLDVDPGYGRV	158
DB	64	LEGINTSLPTLGAGESAFNIHFWDGSMGIPGAFYIKNYMQVEFFLKSLTLEAISNOGTI	123
QY	159	HFDCHSWTVPSGRKKOEIFEANHVLPSOTMPLKYREELWNLRGDTGERKEWDRI	218
DB	124	RVCNCSSWNTKLKYSVRIFANHYTVPSETPAFLVSIREELUKSURGNGTGGERKEYDRI	183
QY	219	YDYVDVNDIADPDVGDH--REILGTTETEYPYPRRGRTGRPRSRDHYESRLSPIMSLDI	276
DB	184	YDYVDVNDLGNDFDKSEKLARPVLGSSSTFFPYPRRGRTGRGPTVTDPNTEKQ----	238
QY	277	VYPKDENFGHLKNMSDFLYTKALSIKPKLOSIDV--TPNEFDNFKEVDNLFERGFPP	334



CC -!- SIMILARITY: Contains 1 PLAT domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; L35931; AAA64893.1; .  
DR PIR; T05941; T05941.  
DR HSSP; P09186; 1LANH.  
DR InterPro; IPR000907; Lipoxigenase.  
DR InterPro; IPR001024; Lipoxigenase\_LH2.  
DR InterPro; IPR008976; PLAT\_LH2.  
DR Pfam; PF00305; lipoxigenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; FALSE\_NEG.  
DR PROSITE; PS00955; PLAT; 1.  
KW Oxidoreductase; Dioxygenase; Iron; Multigene family.  
FT DOMAIN 34 161  
FT METAL 517 IRON (BY SIMILARITY).  
FT METAL 522 IRON (BY SIMILARITY).  
FT METAL 708 IRON (BY SIMILARITY).  
FT METAL 862 IRON (BY SIMILARITY).  
SQ SEQUENCE 862 AA; 96393 MW; F55954473467BEAA CRC64;  
  
Query Match 52.1%; Score 2438; DB 1; Length 862;  
Best Local Similarity 53.3%; Pred. No. 1.9e-159;  
Matches 463; Conservative 154; Mismatches 225; Indels 26; Gaps 12;  
  
QY 28 GNILDRVSLSGNK---TKGVILMRSNVLPDTEPHSLNLDNFTLGGVSPFLISATH 84  
DB 4 GGLIDTLT--GANKSARLKGTVLMKRVLDLDFGATIIDGIGFELGKGYTCQLISSTA 61  
  
QY 85 TSNDS--RGKYNKAYLERWTSIIPLPAGESVFOINFOWD-ENFGPGAPFIKNGHTSE 141  
DB 62 VDQNGRGKVGAELEQWTSLSLTGTSKGLTDFMEVKLVGPAIVVANNYHSSE 121  
  
QY 142 FFLKSLTLDVDPG-YGRVHFDGNSWVPSGRYKDKRIFFANHVLPSTQPNPLKRYREE 200  
DB 122 FLKLTITLHDVGRGNLTFVANSWYPAANYRSRVFFANDTYLPSQMPAALPYRDDE 181  
  
QY 201 LNNLSGDG-TGERKEMDRYDYVDVNDIADPDVGDHREILGTTETYPYPRSGRTGRPSR 259  
DB 182 LNNLKGDDQGGYQEHDRIRYVDVNDL-----GEGRFLGNSGDHPYPRGRTKRPNA 236  
  
QY 260 RDHNYESRLSPIMSDIYVPKDNFCHLMSDFLGYTLKALSISIKPGLQSFIDVTPNEF 319  
DB 237 SDPSLESRLS--LLAQIYVPRDEKFGHLKTSDFLGYSKAITQGIPLPAVRTYVDTTGEF 294  
  
QY 320 DNFKEVDNLPERGFIP-FNAKTTITEDLTPLFLKALVNDGKELKPTTEVVKDKIG 378  
DB 295 DSFDQIINLYEGIKLPKVALEELRKQFPQLIKDLPVGGDSLLKLPVPHIIQENKQA 354  
  
QY 379 WSTDDEFAREMLAGNPLILRELEAFPPTSKLDPNVGNQNSSTIPEEIRKHLGLDGLTYDE 438  
DB 355 WRTDEFAREVLAGNVPWITELTEFPKPSLDPKSGFDGHTSTIAEHIKNLEGLTVQ 414  
  
QY 439 AKQNRLYIVDFHDMPLVTRM-NATSTKVATRTILLKDDGLTKDLVTELALPHQ 497  
DB 415 ALESNRLYLDHHRFMPFLDVNNLPGNFYATRTFLFLRGDGLTFLATELSEPIIQ 474  
  
QY 498 DQGLGSLKYFPAENG-VOKSTWOLAKAVTVNDVGVYHQLISHWLTHAVLEPFVIATHR 556  
DB 475 GLTTAKSKYITVPVSGVEGWELAKAVAVNDSGWELVSHWLTHAVMEPFVISTNR 534  
  
QY 557 QLSVLPHIHLKLVPHYKQDMFNASARQVLINANGLIETHYPSKYSMELSYLYKDTWF 616  
DB 557 QLSVLPHIHLKLVPHYKQDMFNASARQVLINANGLIETHYPSKYSMELSYLYKDTWF 616

DB 535 HLSVTHPVHKLSPHYRDTMTINALARQTLINAGGIPFMTVPCKFALGMSAVVYKDWKF 594  
QY 617 PQALPNMLMRGLAVESSAPHLRLINDYPAFVNDGLDITWSAIKTWQDYCCLYKDD 676  
DB 595 TEQGLPDDLIRGMVAVEDSPSPYKRVLLVSDYPAADGLAIWHALEQVSVLYAIYPND 654  
QY 677 NAVQNDFELQSWNLRKGHADKHEPWPMPKMTLSLIESCTTIWIASALHAANVFG 736  
DB 655 GVLQGDTEVQAWKTRVREGCDLKDAFWPMQSVPELAKACTIWIIGSALHAANVFG 714  
QY 737 QYPGYILNREPTTSRRFMPEVGTAEYKELSNPEKAFRTICSELQALVSIIEILSK 796  
DB 715 QYFVAGFLPNRTVSRMRPPEGTBEYAELEDRPERAFIHTITISQITQIIGVSLVLSK 774  
QY 797 HASDEVYLGORASIDWTSKTALEAFKFGKLNPEVKNRIMERKNVNLKRSQPVNL 856  
DB 775 HSDDELYLQGRDTPWTSDPKALEVFKFSDRLVIESKVVGMHDPDLKRNNGEPAKFPY 834  
QY 857 TLLVFSNE-----GLTGRGIPNSISI 878  
DB 835 MLLYNTSDHKGAAAGLTAKGIPNSISI 862  
  
RESULT 15  
LOXB\_PHAVU STANDARD; PRT; 741 AA.  
AC P27481;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Lipoxigenase (EC 1.13.11.12) (Fragment).  
OS Phaseolus vulgaris (Kidney bean) (French bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
OX NCBI\_TaxID=3885;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv, Red Mexican; TISSUE=Leaf;  
RX MEDLINE=94003416; PubMed=8400375;  
RA Slusarenko A.J., Meier B.M., Shaw N.;  
RT "Spatial and temporal accumulation of defense gene transcripts in  
RT bean (Phaseolus vulgaris) leaves in relation to bacteria-induced  
RT hypersensitive cell death."; 6:453-466(1993).  
RL Mol. Plant Microbe Interact. 6:453-466(1993).  
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF  
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND  
CC DEVELOPMENT, PEST RESISTANCE, AND SENSATION OR RESPONSES TO  
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING  
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.  
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-  
CC hydroperoxyoctadeca-9,11-dienoate.  
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.  
CC -!- SUBUNIT: Monomer.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
CC -!- SIMILARITY: Contains 1 PLAT domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X63521; CAA45086.1; .  
DR PIR; S18906; S18906.  
DR HSSP; P08170; 2SBL.  
DR InterPro; IPR000907; Lipoxigenase.  
DR InterPro; IPR001024; Lipoxigenase\_LH2.  
DR InterPro; IPR008976; PLAT\_LH2.  
DR Pfam; PF00305; lipoxigenase; 1.



**This Page Blank (uspto)**